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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 22:12:57 ; Search time 8726 Seconds

11261.165 Million cell updates/sec

US-09-892-949-1

Perfect score: 2402
Sequence: 1 ggcacgagtggtgtgcag.....atgagacctggggcctca 2402

IDENTITY_NUC

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	2402	100.0	2402	6	AX365149			AX365149 Sequence
2	2334	97.2	2952	6	BD176872			BD176872 NR10 sp1
3	2334	97.2	5271	6	BD176871			BD176871 NR10 sp1
4	2258.6	94.0	2480	6	AX467333			AX467333 Sequence
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6	2204	91.8	3072	6	BD176873			BD176873 NR10 sp1
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8	2160	89.9	2870	6	BD176874			BD176874 NR10 sp1
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ALIGNMENTS

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LOCUS	AX365149	2402 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0200721.			
ACCESSION	AX365149			
VERSION	AX365149.1	GI:18696908		
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Speicher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L. and Maurer,M.F.			
TITLE	Cytokine receptor zcytor17			

JOURNAL Patent: WO 020721-A 1 03-JAN-2002;

ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

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171. 2369

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CDS

BASE COUNT 713 a 532 c 580 g 577 t
ORIGIN

Query Match 100.0%; Score 2402; DB 6; Length 2402;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION BD178872.1 GI:30016139
VERSION BD178872.1 GI:30016139
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AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
JOURNAL Patent: WO 02077230-A 3 03-OCT-2002;
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MASAKAZU HASEGAWA
OS Homo sapiens (human)
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PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PR 26-MAR-2001 JP 01P 087298

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SOURCE			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1		
AUTHORS	Cosman, D. J., Mosley, B. A., Bird, T. A., Dubose, R. F. and Wiley, S. R.		
TITLE	Hematopoietic receptors hpr1 and hpr2		
JOURNAL	Patent: WO 0229060-A 3 11-APR-2002;		
FEATURES	Immunex Corporation (US)		
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ORIGIN			600 t

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Best Local	Similarity	99.8%	Prod. No. 0		
Matches 2261	Conservative	0	Mismatches	4	Indels
					Gaps
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LOCUS AX467335
DEFINITION Sequence 5 from Patent W00229060.
ACCESSION AX467335
VERSION AX467335.1 GI:21900585
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
TITLE Hematopoietin receptors hpr1 and hpr2
JOURNAL Patent: WO 0229060-A 5 11-APR-2002;
Immunex Corporation (US)
LOCATION/Qualifiers
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ACCESSION BD178873
VERSION BD178873.1 GI:30016140
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3072)
AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
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MASAKAZU HASEGAWA
COMMENT OS Homo sapiens (human)
PN WO 02077230-A/4
PD 03-OCT-2002
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PR 26-MAR-2001 JP 01P 087298
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VERSION
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 AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de
 Sauvage, F. J.
 TITLE A novel type I cytokine receptor is expressed on monocytes, signals
 proliferation, and activates STAT-3 and STAT-5
 JOURNAL J. Biol. Chem. 277 (19), 16831-16836 (2002)
 MEDLINE 21988187
 PUBMED 11877449
 REFERENCE 2 (bases 1 to 2199)
 AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de
 Sauvage, F. J.
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 South San Francisco, CA 94080, USA
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RESULT 8
LOCUS BD178874 2870 bp DNA linear PAT 16-APR-2003
DEFINITION NR10 splicing variants.
ACCESSION BD178874
VERSION BD178874.1 GI:30016141
KEYWORDS WO 02077230-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2870)
AUTHORS Meda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
JOURNAL Patent: WO 02077230-A 5 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MEDA,NORIKO YAGUCHI,
MASAKAZU HASEGAWA
OS Homo sapiens (human)
PN WO 02077230-A/5
PD 03-OCT-2002

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PF 22-MAR-2002 WO 2002JP002769
PR 26-MAR-2001 JP 01P 087298
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C12N5/10,
PC C12P21/02,G01N33/15,G01N33/50,G01N33/53
CC NR10 splicing variants
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FT CDS Location/Qualifiers
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Best Local Similarity 96.5%; Pred. No. 0;
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QY 129 CAAAACATTCCTCTCCCGCCAGCCCTTCATGCTTAACCTGGGGAGATGGACCTGGGCA 188
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QY 189 CTGTGATGTCCTCCCTCCTCCTGCAAAATTCAGCTGCGACGTCGCCAGCTAAACCTGAG 248
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Db 121 CTGTGATGTCCTCCCTCCTCCTGCAAAATTCAGCTGCGACGTCGCCAGCTAAACCTGAG 180
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QY 309 GAAACAGATTATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAACATGAT 368
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QY 609 CCTGAGTTGGCGGCTGTTTATCTGATTTAAATATACACACTTCGATTGAGGACGTAAC 668
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DB 841 GTGGGGTGTGTATGGAAAGCAAG 900
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DB 901 AACATATGTGTATGTATCCAGAAAGCAACACTTAACCTCAAGAAACATGATGATGATGATGATGAT 960
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DB 961 CAGCAGCTTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1089 TCTCTGTGGAGAGTCTCCAG 1148
DB 1021 TCTCTGTGGAGAGTCTCCAG 1080
QY 1149 CAGTGTGAT 1208
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QY 1209 AGCTGTGCTGTAGACGTGACACCTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
DB 1141 AGCTGTGCTGTAGACGTGACACCTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1269 CCCACACACCTTCTGTGGAGAGT 1328
DB 1201 CCCACACACCTTCTGTGGAGAGT 1260
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DB 1261 AAATTTAAACCTTCTGT 1320
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DB 1321 GCGCAGCCTATTTCCATCAGCAGCTTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1449 ACCAAGGTGAGAGACATGCGGTGAG 1508
DB 1381 ACCAAGGTGAGAGACATGCGGTGAG 1440
QY 1509 AGTGTGAG 1568
DB 1441 AGTGTGAG 1500
QY 1569 GGATTTCTCCAGACAGTCAATTTCCAGATCTTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1628
DB 1501 GGATTTCTCCAGACAGTCAATTTCCAGATCTTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1629 AAGACCTCTTACATTTGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1688
DB 1561 AAGACCTCTTACATTTGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1689 AGCATTAATTTCAAGACATTTGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1748
DB 1621 AGCATTAATTTCAAGACATTTGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1749 ATTGTGTGAG 1808
DB 1681 ATTGTGTGAG 1740
QY 1809 AACAAATTTGATCTATCTGT 1868
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QY 1989 AAGTTGGTGAG 2048
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DB 2139 CCATATTTTGAAG 2198
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RESULT 9

BD178875

LOCUS

BD178875

DEFINITION

NR10 splicing variants.

ACCESSION

BD178875.1

VERSION

GI:30016142

KEYWORDS

WO 02077230-A/6.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 2858)

AUTHORS

Maeda,M., Yaguchi,N. and Hasegawa,M.

TITLE

NR10 splicing variants

JOURNAL

Patient. WO 02077230-A 6 03-OCT-2002.

COMMENT

CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA

OS

Homo sapiens (human)

PN

WO 02077230-A/6

PD

03-OCT-2002

PR

26-MAR-2001 JP 01P 087298

PI

MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC

C12N15/12

C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC

PC

C12P21/02, G01N33/15, G01N33/50, G01N33/53

CC

NR10 splicing variants

FH

key

FT

CDS

FEATURES

source

BASE COUNT

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ORIGIN

1. 2858

Query Match

88.9%

Best Local Similarity

96.0%

Pred. No. 0;

Matches 2240;

Conservative 0;

Mismatches 0;

Indels 94;

Gaps 1;

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Db	121	CTGTGATGCTCCCTCACTCTGCAAAATTCAGCCTGGACCTCTGGCCAGCTTAAGCCTGAG	180
QY	249	AACATTTCTCTGTCTACTACTATAGGAAAAATTTAACTGTGACCTGGAGTCCAGAAAG	308
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QY	369	AATTTGTACAACCAATAGTTCTTACAGTGAATAATGTGCTTCGTGCTCTTTTTCCTTCCA	428
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QY	429	AGAATTAACGATCCCACTAATTTATACATTGAGGTGAGACTGAATAATGGAGATGTGTA	488
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QY	609	CTGTAGTTGGCGCTGTTTTCATCTGATTTAAATACACACTTGATTCAGACAGCTAAC	668
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Db	1648	-----1647	
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OY	1929	AACACAGAGACAGATCTTTAAACCAATGTTCCACCCCCCACTGACAGTGGGTATATGAC	1988
Db	1767	AACACAGAGACAGATCTTTAAACCAATGTTCCACCCCCCACTGACAGTGGGTATATGAC	1826
OY	1989	AAGTTGGTGGGAAGTGGGAATGTTCTGCAACAAATTTTCCACAGATGAAGCCAGAGC	2048
Db	1827	AAGTTGGTGGGAAGTGGGAATGTTCTGCAACAAATTTTCCACAGATGAAGCCAGAGC	1886
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Db	1887	GGTCAGGAAAACAATTTAGAGAGGGGAAAAAAGATGGTATGTGACTGCCCTTCAGAGCCT	1946
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Db	1947	GATGTGCCCCCTGGGGAAAAAGTTTGGAGAGGCTCCCACTGTTTACTGAGATTTCCGCCCA	2006
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Db	2007	AAATCCCAATACATGATTTGAGAGATGCGAAGGGGACCCGCCAGAAAGCCAAAGAGACAG	2066
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RESULT 10
AA365193 2529 bp DNA linear PAT 15-FEB-2002
LOCUS DEFINITION Sequence 45 from Patent WO0200721.
AA365193
ACCESSION
VERSION AX365193.1 GI:18696949
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuljper, J.L. and Maurer, M.F. Cytokine receptor zcytor17 Patent: WO 0200721-A 45 03-JAN-2002;
AUTHORS JOURNAL ZymoGenetics, Inc. (US)
FEATURES
Source Location/Qualifiers
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BASE COUNT 764 a 530 c 576 g 659 t
ORIGIN

Query Match 86.4% Score 2075; DB 6; Length 2529;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGTGTGTGCAATGAAAAATGAGACAGAGGAGAGTGTACGTTGTCCACCTGAC 60
Oy 70 TGGGATGTGATGAGGCACTCAAGTTTTTACACGCGCATGTGTCTGTGAATGCCG 129
Db 61 TGGGATGTGATGAGGCACTCAAGTTTTTACACGCGCATGTGTCTGTGAATGCCG 120
Oy 130 AAAACATTTCTCTCCCGACGCTTCATGTGTTAACTGCGGATGATGTGGACCTGGGAC 189
Db 121 AAAACATTTCTCTCCCGACGCTTCATGTGTTAACTGCGGATGATGTGGACCTGGGAC 180
Oy 190 TGTGATGTCTCCCTCACTGTGCAAAATTCAGCTGGACGTCTGGACACCTAAGCCTGGA 249
Db 181 TGTGATGTCTCCCTCACTGTGCAAAATTCAGCTGGACGTCTGGACACCTAAGCCTGGA 240

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Oy 310 AAACAGTTATACCCAGTACACAGTAAAGACACTTACGCTTTTGGAAAAACATGTATA 369
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Oy 370 AFTGTACAAACCAATGTTCTCAAGTGAATAATCGGCTTGGCTCTTTTCCCTCCAA 429
Db 361 AFTGTACAAACCAATGTTCTCAAGTGAATAATCGGCTTGGCTCTTTTCCCTCCAA 420
Oy 430 GAATTAACGATCCACATATTAATATACATTTGAGGTGAAGCTGAATAAGAGATGGTATA 489
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Oy 550 TTTTCCGCTGTAACACAGTTTGGGATCAACGAAATGATCAATGATGATGAAGC 609
Db 541 TTTTCCGCTGTAACACAGTTTGGGATCAACGAAATGATCAATGATGATGAAGC 600
Oy 610 CTGAGTTGGCCCTGTTTCATCTGATTTAAATACACATTCGATTCAGACAGTCAACA 669
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Oy 670 GTACAGCTGATGGAATCAACTTCGTAAGAACCGTAAGGATTAACCAACAGTACA 729
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Db 721 ACCTCAGCGGGCTGAGGCTTTTACAGAAATGTATGATGCTCTGCGATGTCGGGTCAAG 780
Oy 790 AGTCAAACTTGTGAGTACTGAGACCAAGAAAAATGGGATGACTGAGAGCAAGCTC 849
Db 781 AGTCAAACTTGTGAGTACTGAGACCAAGAAAAATGGGATGACTGAGAGCAAGCTC 840
Oy 850 CATGAGGCTGGAAGTGTGAGAGTCCCTGAAACCAAGCTGAGCGGATGGAAGAACGAC 909
Db 841 CATGAGGCTGGAAGTGTGAGAGTCCCTGAAACCAAGCTGAGCGGATGGAAGAACGAC 900
Oy 910 TGGGTTTGTGGAAGAGCAAGAGAGAGGCGGCTGCTGAGAGAAACACTTGGCTACA 969
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Oy 970 ACATATGCTACTATCCAGAAAGCAACACTAACCTACAGAAACAATGACACTACTAAC 1029
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Db 1021 AGCAGCTTGAAGTGCATCTGGAGGCGAGGAGCTTTGGTGTCTATGATTTCTATATTT 1080
Oy 1090 CTCTTGGGAAGTCTCAGTGGCCACCGCTGAGAGATTCACGATTTCAAGAAAAATCATATTC 1149
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Oy 1270 CCACACACCTTCTCGGGAATCTGTGCTCAGGCGACCAACCTGAGACATTCAGCAAGATA 1329
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Db	1321	AAAAAAAACTTTCTGGTGTATACATCTCTGTATCCAAAGTTGACATGACAAATGTC	1380
QY	1390	GGAGGCATATTCATCCAGGCTTATGSCAAAGAGGCGTTCCATCGAAGGTCCTGAGA	1449
Db	1381	GGAGGCATATTCATCCAGGCTTATGSCAAAGAGGCGTTCCATCGAAGGTCCTGAGA	1440
QY	1450	CCAAGGTGAGAACATTTGGCGGTGAGAGCGGTCAAGCATGATGGAAGAGATTCGCCAGA	1509
Db	1441	CCAAGGTGAGAACATTTGGCGGTGAGAGCGGTCAAGCATGATGGAAGAGATTCGCCAGA	1500
QY	1510	GTCAGAGAAAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAAGTGGAAG	1569
Db	1501	GTCAGAGAAAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAAGTGGAAG	1560
QY	1570	GATTTCCAGAGACAGTCAATTCAGACATCTTGAGTGGCGCTGGAGTCCCTGAACGAA	1629
Db	1561	GATTTCCAGAGACAGTCAATTCAGACATCTTGAGTGGCGCTGGAGTCCCTGAACGAA	1620
QY	1630	AGACCTCTTACATTTGTTCAAGTCATGGCCAGCACCATGCTGGGGAGAACACGCGACCA	1689
Db	1621	AGACCTCTTACATTTGTTCAAGTCATGGCCAGCACCATGCTGGGGAGAACACGCGACCA	1680
QY	1690	GCAATAATTTCAAGACATTTGTCACTCATGTCTTTGAGATTATCCCTCATTAATCTCTGA	1749
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QY	1750	TTGGTGGAGGCTCTTATCTCATTAATCTGACAGTGGCATATGGCTCTTAAAAACCA	1809
Db	1741	TTGGTGGAGGCTCTTATCTCATTAATCTGACAGTGGCATATGGCTCTTAAAAACCA	1800
QY	1810	ACAAATTTGACTCATCTGTGTGGGCCACCGTCCCAACCTGCTGAGAAAGTATGACCA	1869
Db	1801	ACAAATTTGACTCATCTGTGTGGGCCACCGTCCCAACCTGCTGAGAAAGTATGACCA	1860
QY	1870	CATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGACTCTGTA	1929
Db	1861	CATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGACTCTGTA	1920
QY	1930	ACACAGAGACAGAGATTTTAAACCATGTTCCACCCCGCAAGTGTGATGTTTACA	1989
Db	1921	ACACAGAGACAGAGATTTTAAACCATGTTCCACCCCGCAAGTGTGATGTTTACA	1980
QY	1990	AGTTGGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCGAGAAG	2049
Db	1981	AGTTGGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCGAGAAG	2040
QY	2050	GTCAGGAAAAAATTTAGAGAGGAAAAAATGGG	2084
Db	2041	GTCAGGAAAAAATTTAGAGAGGAAAAAATGGG	2075

RESULT 11
BD178870
LOCUS BD178870 4315 bp DNA linear PAT 16-Apr-2003
DEFINITION NR10 splicing variants.
ACCESSION BD178870
VERSION BD178870.1 GI:30016137
KEYWORDS WO 02077230-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4315)

REFERENCE
AUTHORS Meda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
JOURNAL Patent: WO 02077230-A 1 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MEDA,NORIKO YAGUCHI,
MASAKAZU HASEGAWA
OS Homo sapiens (human)
PN WO 02077230-A/1
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769

COMMENT

QY	69	CTGGGAATGTGACATCAGACACCTCAATTTTTCACACGCGCATGTCTGTAATGCC	128
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Db	61	CAAAACATTTCTCTCTCCCGACCTTCATGTGTTAACCTGGGAGATGATGGACCTGGCA	120
QY	189	CTGTGGATGCTCCCTCAGCTCTGCAATTCAGCCCTGACCTCTGCCAGCTAACCTGAG	248
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QY	249	AACATTCCTGTGCTCTCTACTACTATAGAGAAATTTTACCTGCACTTGGATCCAGGAAG	308
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QY	309	GAACACGATTAATCCAGTACACAGTTAAGAGAACTTACCTTTTGAGAGAAAAACATGAT	368
Db	241	GAACACGATTAATCCAGTACACAGTTAAGAGAACTTACCTTTTGAGAGAAAAACATGAT	300
QY	369	AATTGTACAACCAATAGTTTACAGTGAAGAAATCGTCTGTCCTTTTTCCTTCCA	428
Db	301	AATTGTACAACCAATAGTTTACAGTGAAGAAATCGTCTGTCCTTTTTCCTTCCA	360
QY	429	AGATTAACGATCCCGAGTAATTTATACATGAGTGAAGCTGAAGTGAAGATGAGTGA	488
Db	361	AGATTAACGATCCCGAGTAATTTATACATGAGTGAAGCTGAAGTGAAGATGAGTGA	420
QY	489	ATTAAATCTCATATGACATCTGAGATTTAGAGAACTAGCAAAACCTGAACCTGAAG	548
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QY	549	ATTTTCGGGTGAACACAGTTTGGGCATCAACGAATGATTCAAATTTGAATGATTAAG	608
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QY	609	CTGAGTTGGCGCCTGTTTCATCTGATTTTAAATATACACCTTGATTCAGAGACGTCAAC	668
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QY	789	GAGTCAAGATTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	848
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Oy 1809 AACAAATTTGACTATCTGTGTTGGCCACCGCTTCCCAACCTGCTGAAAGATATAGCC 1868
Db 1741 AACAAATTTGACTATCTGTGTTGGCCACCGCTTCCCAACCTGCTGAAAGATATAGCC 1800
Oy 1869 ACATGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGACTCTGTG 1928
Db 1801 ACATGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGACTCTGTG 1860
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Db 1921 AAGTTGGGTGAGACTTTGGGAATCTGTGCAAGAAATTTTACAGATGAACCCAGAACG 1980
Oy 2049 GGTGAGGAAACAAATTTAGGAGGGGGAAGATGGG 2084
Db 1981 GGTGAGGAAACAAATTTAGGAGGGGGAAGATGGG 2016

RESULT 12
BD178876
LOCUS BD178876
DEFINITION NR10 splicing variants.
ACCESSION BD178876.1 GI:30016143
VERSION WO 02077230-A/7.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2776)
AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
JOURNAL Patent: WO 02077230-A 7 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YAGUCHI,
MASAKAZU HASEGAWA
OS Homo sapiens (human)
PN WO 02077230-A/7
PD 03-OCT-2002
PE 22-MAR-2002 WO 2002JP022769
PR 26-MAR-2001 JP 01P 087298
PI MASATSUGU MAEDA,NORIKO YAGUCHI,MASAKAZU HASEGAWA PC
C12N15/12,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10, PC
C12P21/02,G01N33/15,G01N33/50,G01N33/53
CC NR10 splicing variants
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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BASE COUNT 776 a 646 c 692 g 662 t

Query Match 82.1%; Score 1972; DB 6; Length 2776;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2158; Conservative 0; Mismatches 0; Indels 176; Gaps 1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 2119)
AUTHORS Maeda, M. and Yaguchi, N.
TITLE Novel hemopoietin receptor protein, NR10
JOURNAL Patent: WO 0075314-A 14-DEC-2000;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC., MASATSUGU
MAEDA, NORIKO YAGUCHI
OS Homo sapiens (human)
COMMENT PN WO 0075314-A/14
PD 14-DEC-2000
PE 01-JUN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 155797, 30-JUL-1999 JP 99P 217797 PI
MASATSUGU MAEDA, NORIKO YAGUCHI
PC C12N15/12, C12N5/10, C07K14/715, C07K16/28, C12P21/02, G01N33/53,
PC G01N33/56
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KEY CDS
LOCATION/Qualifiers (11) . (1996).
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ORIGIN
Query Match 81.1%; Score 1947; DB 6; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0;
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Db	1817	GACAGATCTTTAAACCATGTTCCACCACCAGTGACAGAGTGTGATGACAAGTTGGT	1876	
OY	1998	GTCGAATTTGGGAATGTTTCGAAGAAATTTTTCACAGATGAAGCCGAGAGGGTCAAGAA	2057	
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Db	1937	AACCAATTTAGAGGGGAAAAAAGATGGG	1963	
RESULT 14				
LOCUS	AX365201	2903 bp	DNA linear PAT 15-FEB-2002	
DEFINITION	Sequence 53 from Patent WO0200721.			
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REFERENCE	1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kujper, J.L. and Maurer, M.F. Cytokine receptor zcytor17 Patent: WO 0200721-A 53 03-JAN-2002; ZymoGenetics, Inc. (US) Location/Qualifiers			
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JOURNAL				
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TITLE Maeda,M. and Yaguchi,N.
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PI Sprechter CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
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DR WPI: 2002-090519/12.
DR P-FSDB: ABB05730.
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PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Claim 2: Page 161-166; 235pp: English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antineoplastic, antidiabetic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
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AC AB083365;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:5.
XX
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 7..2301
XX FT /*tag= a
XX FT /product= "NR10.4"
XX
XX MO200277230-1.
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PD 03-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-JP02769.
XX
XX 26-MAR-2001; 2001JP-0087298.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M.
XX
XX WPI; 2003-018925/01.
XX
XX P-PSDB; ABP54365.
XX
XX NR10 splicing variants of haematopoietin receptor proteins and encoded
PT genes; applicable in searching haematopoietic factors and developing
PT remedies for immunological and haematopoietic diseases
XX
XX Claim 1; Fig 7-9; 250p; Japanese.
XX
XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate
CC in in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence encodes the human NR10.4 protein
CC from the present invention.
XX
XX Sequence 2952 BP; 821 A; 688 C; 727 G; 716 T; 0 other:
S0
Query Match 97.2%; Score 2334; DB 25; Length 2952;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 CTGGGAATGTGCATCAGGACCACTCAAGTTTTCACACAGGCGATGCTGTGAATGCC 128
    |||||||
Db 1 CTGGGAATGTGCATCAGGACCACTCAAGTTTTCACACAGGCGATGCTGTGAATGCC 60
QY 129 CAAACATTTCTCTCTCCCGACGCTTCATGTGTTAACCTGGGAGATGTGGACTGGGCA 188
    |||||||
Db 61 CAAACATTTCTCTCTCCCGACGCTTCATGTGTTAACCTGGGAGATGTGGACTGGGCA 120
QY 189 CTGTGATGTGCCCTCAGTCTGCAATTCAGCTGCGAGCTGCCAGTAAAGCTGAG 248
    |||||||
Db 189 CTGTGATGTGCCCTCAGTCTGCAATTCAGCTGCGAGCTGCCAGTAAAGCTGAG 248
QY 121 CTGTGATGTGCCCTCAGTCTGCAATTCAGCTGCGAGCTGCCAGTAAAGCTGAG 180
    |||||||
Db 121 CTGTGATGTGCCCTCAGTCTGCAATTCAGCTGCGAGCTGCCAGTAAAGCTGAG 180
QY 249 AACATTTCTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGAAAG 308
    |||||||
Db 249 AACATTTCTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGAAAG 308
QY 181 AACATTTCTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGAAAG 240
    |||||||
Db 181 AACATTTCTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGAAAG 240
QY 309 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAATCATGAT 368
    |||||||
Db 309 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAATCATGAT 368
QY 241 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAATCATGAT 300
    |||||||
Db 241 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAATCATGAT 300
QY 369 AATGTACACCAATAGTCTACAGAGTGAAGAAATGCTGCTGCTTTTTCCTTCCA 428
    |||||||
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QY 301 AATGTACACCAATAGTCTACAGAGTGAAGAAATGCTGCTGCTTTTTCCTTCCA 360
    |||||||
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QY 429 AGAATTAACGATCCAGATTAATTAATACATGAGTGAAGTGAAGTGAAGTGAAGTGA 488
    |||||||
Db 429 AGAATTAACGATCCAGATTAATTAATACATGAGTGAAGTGAAGTGAAGTGAAGTGA 488
QY 361 AGAATTAACGATCCAGATTAATTAATACATGAGTGAAGTGAAGTGAAGTGAAGTGA 420
    |||||||
Db 361 AGAATTAACGATCCAGATTAATTAATACATGAGTGAAGTGAAGTGAAGTGAAGTGA 420
QY 489 ATTAAATCTCATATGACATACCTGAGATTAAGAACATAGCGAAACCTGAACCTTAAG 548
    |||||||
Db 489 ATTAAATCTCATATGACATACCTGAGATTAAGAACATAGCGAAACCTGAACCTTAAG 548
QY 421 ATTAAATCTCATATGACATACCTGAGATTAAGAACATAGCGAAACCTGAACCTTAAG 480
    |||||||
Db 421 ATTAAATCTCATATGACATACCTGAGATTAAGAACATAGCGAAACCTGAACCTTAAG 480
QY 549 ATTTCGCGTGAAGACAGTTTGGGATCAACAGATGATTAATTAATGAATGAATGAAG 608
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Db 549 ATTTCGCGTGAAGACAGTTTGGGATCAACAGATGATTAATTAATGAATGAATGAAG 608
QY 481 ATTTTCGCGTGAAGACAGTTTGGGATCAACAGATGATTAATTAATGAATGAATGAAG 540
    |||||||
Db 481 ATTTTCGCGTGAAGACAGTTTGGGATCAACAGATGATTAATTAATGAATGAATGAAG 540
QY 609 CCTGAGTTGGCGCTGTTTCACTGATTTAAATATACACACTTCGATTGAGACAGTCAAC 668
    |||||||
Db 609 CCTGAGTTGGCGCTGTTTCACTGATTTAAATATACACACTTCGATTGAGACAGTCAAC 668
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Db 541 CCTGAGTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGCAGCTCAAC 600
Oy AGTACACAGCTGGATGGAAGTCACTGCTAGAACCGTAAGGATTAATAACCAACGCTAC 728
Db 601 AGTACACAGCTGGATGGAAGTCACTGCTAGAACCGTAAGGATTAATAACCAACGCTAC 660
Oy 729 AACCTCAGGGGGCTGACAGCTTTTACAGAAATATGTCATAGCTGTCGATGTCGGTCAAG 788
Db 661 AACCTCAGGGGGCTGACAGCTTTTACAGAAATATGTCATAGCTGTCGATGTCGGTCAAG 720
Oy 789 GAGTCAAAAGTCTGAGAGTGAAGTGAAGGCAAGAAAAATGGAAATGACTGAGGAAGAACT 848
Db 721 GAGTCAAAAGTCTGAGAGTGAAGTGAAGGCAAGAAAAATGGAAATGACTGAGGAAGAACT 780
Oy 849 CCATGTGGCCCTGAGAACTGTGAGAGTCTTGAACACAGCTGAGCGGATGAGGAAGGCA 908
Db 781 CCATGTGGCCCTGAGAACTGTGAGAGTCTTGAACACAGCTGAGCGGATGAGGAAGGCA 840
Oy 909 GTGGCGTTGTTATGGAAGAGGCAAGAGAGCCCACTGCTTAGAGAAAACTTGGCTAC 968
Db 841 GTGGCGTTGTTATGGAAGAGGCAAGAGAGCCCACTGCTTAGAGAAAACTTGGCTAC 900
Oy 969 AACATATGCTACTATCCAGAAAGCAACACTAATCTCAGAGAAACATGATGACTACTAAC 1028
Db 901 AACATATGCTACTATCCAGAAAGCAACACTAATCTCAGAGAAACATGATGACTACTAAC 960
Oy 1029 CAGCAGCTTGAACCTGCTGGAGGCGAGAGCTTTTGGGCTGCTCATGATTTCTTATAT 1088
Db 961 CAGCAGCTTGAACCTGCTGGAGGCGAGAGCTTTTGGGCTGCTCATGATTTCTTATAT 1020
Oy 1089 TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTT 1148
Db 1021 TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTT 1080
Oy 1149 CAGTGCANTGAGTATCAGCAGGCTGCTGCTGAGGACGAGCTAGTGTGTAAGTGGCAA 1208
Db 1081 CAGTGCANTGAGTATCAGCAGGCTGCTGCTGAGGACGAGCTAGTGTGTAAGTGGCAA 1140
Oy 1209 AGCTCTGCTAGACGTAACACTTGGATGATTAATGTTCCGATGTGGACTCAGAG 1268
Db 1141 AGCTCTGCTAGACGTAACACTTGGATGATTAATGTTCCGATGTGGACTCAGAG 1200
Oy 1269 CCCACACCCCTTCTGGGAATCTGTCTCAGGCCACAGAACTGAGCATCAGCAAGAT 1328
Db 1201 CCCACACCCCTTCTGGGAATCTGTCTCAGGCCACAGAACTGAGCATCAGCAAGAT 1260
Oy 1329 AAATTAACCTTCTGGTGTATACATCTGTGTATCCATGATCCAGTTGCATGACAAAGTT 1388
Db 1261 AAATTAACCTTCTGGTGTATACATCTGTGTATCCATGATCCAGTTGCATGACAAAGTT 1320
Oy 1389 GCGAGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCAGAAAGTCTGAG 1448
Db 1321 GCGAGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCAGAAAGTCTGAG 1380
Oy 1449 ACCAAGTGGGAACATTTGGCGTAAGACGCTCAGATCAGATGAGAAAGAGATTCACAG 1508
Db 1381 ACCAAGTGGGAACATTTGGCGTAAGACGCTCAGATCAGATGAGAAAGAGATTCACAG 1440
Oy 1509 AGTGAAGAAAGGCTATCATCTGCACTACACCATCTTTTACCAAGCTGAAAGGTGAAAA 1568
Db 1441 AGTGAAGAAAGGCTATCATCTGCACTACACCATCTTTTACCAAGCTGAAAGGTGAAAA 1500
Oy 1569 GGATTTCCAAAGACAGTCAATTCAGCATCTTGCAGTACGGCTGAGATCCCTGAAAGCA 1628
Db 1501 GGATTTCCAAAGACAGTCAATTCAGCATCTTGCAGTACGGCTGAGATCCCTGAAAGCA 1560
Oy 1629 AAGACCTTTACATTTGTCAGGTATGCGCAGACACAGTGTGGGGAAACCAACGGGACC 1688
Db 1561 AAGACCTTTACATTTGTCAGGTATGCGCAGACACAGTGTGGGGAAACCAACGGGACC 1620
Oy 1689 AGCATAAATTTCAAGACATGTCTATAGTGTCTTTAGANTATCCATTAATCTTCTGTG 1748
Db 1621 AGCATAAATTTCAAGACATGTCTATAGTGTCTTTAGANTATCCATTAATCTTCTGTG 1680

Oy 1749 ATGTGTGAGGCTCTCTATTCATATTCATATCCGACAGTGGGATATGGTCTCAAAAAACC 1808
Db 1661 ATGTGTGAGGCTCTCTATTCATATTCATATCCGACAGTGGGATATGGTCTCAAAAAACC 1740
Oy 1809 AACAAATGACTCATCTGTGTGGCCACCGTTCCCAACCCCTGTAAGTATATAGCC 1868
Db 1741 AACAAATGACTCATCTGTGTGGCCACCGTTCCCAACCCCTGTAAGTATATAGCC 1800
Oy 1869 ACATGGCATGAGATGATTTCAAGATATAGCTAAACCTGAAAGAGTCTGATGACTGTG 1928
Db 1801 ACATGGCATGAGATGATTTCAAGATATAGCTAAACCTGAAAGAGTCTGATGACTGTG 1860
Oy 1929 AACACAGAGACAGATCTTAAACCATATGTTCCACCCCACTGACAAATGTTGATGAC 1988
Db 1861 AACACAGAGACAGATCTTAAACCATATGTTCCACCCCACTGACAAATGTTGATGAC 1920
Oy 1989 AAGTTGTGTGAACCTTGGGAATGTCTGCAAGAAATTTTTCACAGATGAAGCAGAACG 2048
Db 1921 AAGTTGTGTGAACCTTGGGAATGTCTGCAAGAAATTTTTCACAGATGAAGCAGAACG 1980
Oy 2049 GGTGAGGAAACATTTTAGAGGGGAAAGATGGTATGTGACTGCGCTTCAAGGCT 2108
Db 1981 GGTGAGGAAACATTTTAGAGGGGAAAGATGGTATGTGACTGCGCTTCAAGGCT 2040
Oy 2109 GATTGTCCCTGGGGAAAAAGTTTGGAGAGCTCCAGTTTCACTGAGATTCGGCCGAGA 2168
Db 2041 GATTGTCCCTGGGGAAAAAGTTTGGAGAGCTCCAGTTTCACTGAGATTCGGCCGAGA 2100
Oy 2169 AAATCCCAATACCTACGTTTCAGAGATGCCAGAGGGGACCCGCCAGAAACCAAGAGAG 2228
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Oy 2229 CTCTCTTTTGTGGTCAAAAGTTTATGACAGATATCTGTGTGAGGAAGAGCCCAAT 2288
Db 2161 CTCTCTTTTGTGGTCAAAAGTTTATGACAGATATCTGTGTGAGGAAGAGCCCAAT 2220
Oy 2289 CCATATTTGAAAAAATTCAGTACAGCAGCAGGAAATTTCTGTGTGAAAAAATTCAGAG 2348
Db 2221 CCATATTTGAAAAAATTCAGTACAGCAGCAGGAAATTTCTGTGTGAAAAAATTCAGAG 2280
Oy 2349 CACACCAAGGAGAGTCTAAATCCGACCATATGACATGAGAGCCCTGGGGCTCA 2402
Db 2281 CACACCAAGGAGAGTCTAAATCCGACCATATGACATGAGAGCCCTGGGGCTCA 2334

RESULT 3
AB083364
ID AB083364 standard; cDNA: 5271 BP.
XX
AC AB083364;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:3.
XX
KW NR10: splicing variant; haematopoietic receptor; immunomodulator;
KW haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2301
FT /tag= a
FT /product= "NR10.4"
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002W0-JP02769.
XX

PR 26-MAR-2001; 2001JP-0087298.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M.
XX
DR WPI; 2003-018925/01.
XX P-PSDB; ABP54364.
PT NR10 splicing variants of hematopoietin receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases
XX
XX Claim 1; Fig 4-5; 250pp; Japanese.
XX
XX The present invention describes haematopoietic receptor NR10 splicing
XX variants (I). (I) have immunomodulator and haemostatic activities. The
XX proteins and encoded genes are applicable in searching for novel
XX haematopoietic factors, and developing remedies for immunological and
XX haematopoietic diseases. The haematopoietin receptor genes participate
XX in in vivo immunomodulation and haematopoietic cell regulation, and in
XX the search for haematopoietic factors capable of functionally binding
XX to the receptors. The present sequence encodes the human NR10.4 protein
XX from the present invention.
SQ
Sequence 5271 BP; 1312 A; 1302 C; 1318 G; 1339 T; 0 other;
Query Match 97.2%; Score 2334; DB 25; Length 5271;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
69 CTGGGAATGTGCATCAGCACTCAAGTTTTCACGAGCAGTGTCTGTGAATGCC 128
1 CTGGGAATGTGCATCAGCACTCAAGTTTTCACGAGCAGTGTCTGTGAATGCC 60
129 CAAACACTTCTCTCTCCCGACCTTCACTGTGTTAACTGGGGATGATGAGCTGGCA 188
61 CAAACACTTCTCTCTCCCGACCTTCACTGTGTTAACTGGGGATGATGAGCTGGCA 120
189 CTGTGATGTGCTCCCTCAGTCTGCAATTCAGCTGAGCTGCTGCGACGTAACCTGAG 248
121 CTGTGATGTGCTCCCTCAGTCTGCAATTCAGCTGAGCTGCTGCGACGTAACCTGAG 180
249 AACATTTCTGTGTCTACTACTATAGAAAAATTAACTGCACTTGAGAGTCCAGAAAG 308
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309 GAAACCGATTATCCCGATACAGATTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 368
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369 AATTGTCAACCAATAGTTCTACAACTGAAATGCTCTGCTCTTTTCTTCTTCCA 428
301 AATTGTCAACCAATAGTTCTACAACTGAAATGCTCTGCTCTTTTCTTCTTCCA 360
429 AGAATAAGCATCCCGATTAATATACATTGAGGTGAGAGCTGAAATGAGATGTGTA 488
361 AGAATAAGCATCCCGATTAATATACATTGAGGTGAGAGCTGAAATGAGATGTGTA 420
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421 ATTTAAATCTGATATGATATGATGAGATGAGAGTAACTGAGAACTGAAACCTGAG 480
549 ATTTTCGCTGGAACCAAGTTTGGGATCAAAAGATGATTCAAATTTGATGATTAAG 608
481 ATTTTCGCTGGAACCAAGTTTGGGATCAAAAGATGATTCAAATTTGATGATTAAG 540
609 CCTGAGTTGGCGCTGTTTCATCTGATTTAAATATACACTTCGATTCAGACAGTCAAC 668
541 CCTGAGTTGGCGCTGTTTCATCTGATTTAAATATACACTTCGATTCAGACAGTCAAC 600
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TT

601 AGTACAGCTGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
729 AACCTACAGGAGGCTGACAGCTTTTACAGAAATATGATGATGATGATGATGATGATGATGAT 788
661 AACCTACAGGAGGCTGACAGCTTTTACAGAAATATGATGATGATGATGATGATGATGATGAT 720
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721 GAGTCAAAAGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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781 CCATGTGCTGTGAGTGTGAGAGTCTGTAACACAGTGTGAGGAGTGTGAGAGGCA 840
909 GTGCGGTTGTTATGAGAAAGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 968
841 GTGCGGTTGTTATGAGAAAGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
969 AACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
901 AACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
1029 CAGAGCTTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1088
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1089 TCTCTTGGGAAAGTCTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1148
1021 TCTCTTGGGAAAGTCTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
1149 CAGTGCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1208
1081 CAGTGCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
1209 AGCTCTGCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
1141 AGCTCTGCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
1269 CCCGACACCCCTTCTCTGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1328
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1329 AAATTTAAACCTTCTCTGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1388
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1449 ACCAAGGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1508
1381 ACCAAGGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1509 AGTGAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1568
1441 AGTGAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1569 GGATTTCCCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1628
1501 GGATTTCCCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1629 AAGACCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1688
1561 AAGACCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1689 AGCATTAATTTCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1748
1621 AGCATTAATTTCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1749 ATTGGTGGAGGCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1808
1681 ATTGGTGGAGGCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740

OY 2178 TACCTACCTGAGATGCGAGAGGAGCCGCCAGAACCAAGACACTTCTCTT 2237
DB 2178 TACCTACCTGAGATGCGAGAGGAGCCGCCAGAACCAAGACACTTCTCTT 2237
OY 2238 TCTGCTCAAGTTTGTACGACATCATCTGTGTGAGAGAGACCCCAATTCATTTG 2297
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DB 2298 AAAAATTGAGTACGAGCCAGGAAATTTCTGTGTGAGAGAGACCCCAATTCATTTG 2357
OY 2358 GGAGAGTCTTAATGCGACATAGACACCCCTGCGGCTCA 2402
DB 2358 GGAGAGTCTTAATGCGACATAGACACCCCTGCGGCTCA 2402
RESULT 5
ABQ83366
ID ABQ83366 standard; cDNA: 3072 BP.
AC ABQ83366;
XX 20-JAN-2003 (first entry)
DT 20-JAN-2003 (first entry)
DE Human NR10.5 splicing variant encoding cDNA SEQ ID NO:7.
XX
XX
KW NR10: splicing variant: haematopoietin receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 7..1890
FT /tag= a
FT /product= "NR10.5"
XX
XX
PN WO20027230-A1.
PD 03-OCT-2002.
XX
XX
PF 22-MAR-2002; 2002WO-JP02769.
XX
XX
PR 26-MAR-2001; 2001JP-0087298.
XX
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
XX
DR WPI: 2003-018925/O1.
DR P-PSDB: ABP54366.
XX
XX
PT NR10 splicing variants of haematopoietin receptor proteins and encoded
PT genes, applicable in searching haematopoietic factors and developing
PT remedies for immunological and haematopoietic diseases -
XX
XX
PS Claim 1; Fig 10-12; 250pp; Japanese.
XX
XX
CC The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (i) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence encodes the human NR10.5 protein
CC from the present invention.
XX
XX
SO Sequence 3072 BP; 849 A; 721 C; 755 G; 747 T; 0 other:
Query Match 91.8%, Score 2204; DB 25; Length 3072;

Best Local Similarity 95.1%; Pred. No. 0;
Matches 2334; Conservative 0; Mismatches 0; Indels 120; Gaps 1;
OY 69 CTGGGAATGTGCATCAGCAACCTAAGTTTTCACACAGCATGTGTCTGAATGCC 128
DB 1 CTGGGAATGTGCATCAGCAACCTAAGTTTTCACACAGCATGTGTCTGAATGCC 60
OY 129 CAACAACATTCCTCTCCACACCTTCATGTGTAACTGGGGAGATGTGGACCTGGGCA 188
DB 61 CAACAACATTCCTCTCCACACCTTCATGTGTAACTGGGGAGATGTGGACCTGGGCA 120
OY 189 CTGTGATGCTCCCTCAGCTCTGCAAAATTCAGCTGAGCTGTGCCAGCTAAGCTGAG 248
DB 121 CTGTGATGCTCCCTCAGCTCTGCAAAATTCAGCTGAGCTGTGCCAGCTAAGCTGAG 180
OY 249 AACATTTCTGTCTGTCTACTATATAGAGAAAATTTAACTGTCACTGTGAGAGTCCAGGAAG 308
DB 181 AACATTTCTGTCTGTCTACTATATAGAGAAAATTTAACTGTCACTGTGAGAGTCCAGGAAG 240
OY 309 GAACACAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTGGAGAAAACATGAT 368
DB 241 GAACACAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTGGAGAAAACATGAT 300
OY 369 AATTGTACAAACCAATAGTTCTACAGTGAAGTGAATCGTCTGCTCTTTTCTCTTCCA 428
DB 301 AATTGTACAAACCAATAGTTCTACAGTGAAGTGAATCGTCTGCTCTTTTCTCTTCCA 360
OY 429 AGAATTAACGATCCCAATATATATACATTTGAGTGGAGAGCTGAAAATTCAGATGCTGA 488
DB 361 AGAATTAACGATCCCAATATATATACATTTGAGTGGAGAGCTGAAAATTCAGATGCTGA 420
OY 489 ATTAATCTCATATGACATATCTGAGATTTAGAGAACTAGAGAACTGAAACCCATGAG 548
DB 421 ATTAATCTCATATGACATATCTGAGATTTAGAGAACTAGAGAACTGAAACCCATGAG 480
OY 549 ATTTTCGCTGTAACACAGTTTGGCATCAACAGAAATGATTCAAATTTGAATGATTAAG 608
DB 481 ATTTTCGCTGTAACACAGTTTGGCATCAACAGAAATGATTCAAATTTGAATGATTAAG 540
OY 609 CCTGAGTTGGGGCTGTTTCACTGATTTAAATATACACCTTGATTCAGAGACATGATAC 668
DB 541 CCTGAGTTGGGGCTGTTTCACTGATTTAAATATACACCTTGATTCAGAGACATGATAC 600
OY 669 AGTACACAGTGAATGAGATCAACTTGTGTAAGAACGTAAGATTAATAAACCAACGTAC 728
DB 601 AGTACACAGTGAATGAGATCAACTTGTGTAAGAACGTAAGATTAATAAACCAACGTAC 660
OY 729 AACCTACAGGGGGCTGACGCTTTTACAGAAATATGTCAATCTGCGATGTGCGGTCAAG 788
DB 661 AACCTACAGGGGGCTGACGCTTTTACAGAAATATGTCAATCTGCGATGTGCGGTCAAG 720
OY 789 GAGTCAAAAGTTCTGAGATGAGTGAAGCAAGCAAAAAATGGGAATGACTGAGAGAAAGCT 848
DB 721 GAGTCAAAAGTTCTGAGATGAGTGAAGCAAGCAAAAAATGGGAATGACTGAGAGAAAGCT 780
OY 849 CCATGTGCTGTGAGTGTGAGAGTCTGTAAGAACCACTAGAGGGATGGAAGAAGGCCA 908
DB 781 CCATGTGCTGTGAGTGTGAGAGTCTGTAAGAACCACTAGAGGGATGGAAGAAGGCCA 840
OY 909 GTGCGGTTGTTATGAGAAAGCAAGAGAGAGCCCACTCTAGAGAAAACATTTGGCTAC 968
DB 841 GTGCGGTTGTTATGAGAAAGCAAGAGAGAGCCCACTCTAGAGAAAACATTTGGCTAC 900
OY 969 AACATATGATGATATCCAGAAAGCAACATTAACCTCAAGAAACATGAACACTACTAAC 1028
DB 901 AACATATGATGATATCCAGAAAGCAACATTAACCTCAAGAAACATGAACACTACTAAC 960
OY 1029 CAGCAGCTTAACATGATCTGAGAGAGCAAGCTTTGGTGTCTATGATTTCTTAAAT 1088
DB 961 CAGCAGCTTAACATGATCTGAGAGAGCAAGCTTTGGTGTCTATGATTTCTTAAAT 1020
OY 1089 TCTCTTGGAAGTCTCAGTGGCCACCTGAGATTCACATATTCAGAAAATATCATTTT 1148
DB 961 TCTCTTGGAAGTCTCAGTGGCCACCTGAGATTCACATATTCAGAAAATATCATTTT 1088

Db 1021 TCTCTGGGAAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAAGAAAAATCATTT 1080
 Oy 1149 CAGTGCATTTGAGCATGACAGGCTGGTTGCTGAGAACACAGTAGTGGTAATGGCAA 1208
 Db 1081 CAGTGCATTTGAGCATGACAGGCTGGTTGCTGAGAACACAGTAGTGGTAATGGCAA 1140
 Oy 1209 AGCTCTGCTAGACGTGAACACTTGGATGATTTGAATGTTTCCGATGTGTGACTAGAG 1268
 Db 1141 AGCTCTGCTAGACGTGAACACTTGGATGATTTGAATGTTTCCGATGTGTGACTAGAG 1200
 Oy 1269 CCCACCACTTTCTCTGGGAATCTGTGTCTCAGGCCACAGAACTGAGATCCAGCAAGAT 1328
 Db 1201 CCCACCACTTTCTCTGGGAATCTGTGTCTCAGGCCACAGAACTGAGATCCAGCAAGAT 1260
 Oy 1329 AAATTAACCTTTCTGTGCTATACATCTCTGTATCCAAATGTTGCATGACAAAGTT 1388
 Db 1261 AAATTAACCTTTCTGTGCTATACATCTCTGTATCCAAATGTTGCATGACAAAGTT 1320
 Oy 1389 GGGCAGCCATATTTCCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAAAGTCTGAG 1448
 Db 1321 GGGCAGCCATATTTCCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAAAGTCTGAG 1380
 Oy 1449 ACCAAGTGGGAACATTTGGCGTGAAGCGTCAAGATCACATGGAAGAGATTCACAG 1508
 Db 1381 ACCAAGTGGGAACATTTGGCGTGAAGCGTCAAGATCACATGGAAGAGATTCACAG 1440
 Oy 1509 AGTAGAGAAAAGGATCATCTGCACTACACCATCTTTTCCAAAGCTGAAGGTGGAAGA 1568
 Db 1441 AGTAGAGAAAAGGATCATCTGCACTACACCATCTTTTCCAAAGCTGAAGGTGGAAGA 1500
 Oy 1569 GGATTTCTCCAGACAGTCAATTTCCAGCATCTTGCAAGTACGGCGTGGATCCCTGAAAGA 1628
 Db 1501 GGATTTCTCCAGACAGTCAATTTCCAGCATCTTGCAAGTACGGCGTGGATCCCTGAAAGA 1560
 Oy 1629 AAGACCTCTTACATTTGTTCAAGTATGAGCCAGCACAGTGTGGGGGACCAACAGGGAGC 1688
 Db 1561 AAGACCTCTTACATTTGTTCAAGTATGAGCCAGCACAGTGTGGGGGACCAACAGGGAGC 1620
 Oy 1689 AGCATTAATTTCAAGACATTTGTCAATCAAGTGTCTTTGAGATTATCCATTAATCTCTGTG 1748
 Db 1621 AGCATTAATTTCAAGACATTTGTCAATCAAGTGTCTTTGAGATTATCCATTAATCTCTGTG 1680
 Oy 1749 ATTGGTGGAGGCGCTTCTTATTCATTAATCTGACAGAGTGGCATATGTTCTCAAAAAACC 1808
 Db 1681 ATTGGTGGAGGCGCTTCTTATTCATTAATCTGACAGAGTGGCATATGTTCTCAAAAAACC 1740
 Oy 1809 AACCAATTTGACTATCTGTGTGTGGCCACCGTTCCTCAACCTGCTGAAAGTAGTATAGCC 1868
 Db 1741 AACCAATTTGACTATCTGTGTGTGGCCACCGTTCCTCAACCTGCTGAAAGTAGTATAGCC 1800
 Oy 1869 ACATGGCATGAGATGATTTCAA----- 1891
 Db 1801 ACATGGCATGAGATGATTTCAAAGGTTGAGACCTTAGAGCCGGACCTTATTATCACTCA 1860
 Oy 1892 ----- 1891
 Db 1861 CTACATGCCAGTGTCTGGGCTAGGCCCTAGGGATACAATAAGTCACTGTCCCTGC 1920
 Oy 1892 -----GATTAAGCTAAACCTGAAGGAGTCTGATGACTGTGTG 1928
 Db 1921 CATGAGGCCACTTGTGATTTTCTGGATTAAGCTAAACCTGAAGGAGTCTGATGACTGTGTG 1980
 Oy 1929 AACACAGAAAGACAGATCTTAAACCATGTTCCACCCCACTGACAGTGTGTGTGTAC 1988
 Db 1981 AACACAGAAAGACAGATCTTAAACCATGTTCCACCCCACTGACAGTGTGTGTGTAC 2040
 Oy 1989 AAGTTGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCAGAACG 2048
 Db 2041 AAGTTGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCAGAACG 2100
 Oy 2049 GGTCAAGAAAACATTTAGAGGGGGAAGAAATGGGTATGTGACCTGCCCTTCAGGCTT 2108
 Db 2101 GGTCAAGAAAACATTTAGAGGGGGAAGAAATGGGTATGTGACCTGCCCTTCAGGCTT 2160

Oy 2109 GATTGTCCCTGGGAAAGATTTTGAAGAGTCCACATTTACCTGAGATTCGCCCCAGA 2168
 Db 2161 GATTGTCCCTGGGAAAGATTTTGAAGAGTCCACATTTACCTGAGATTCGCCCCAGA 2220
 Oy 2169 AATCCCAATACCTACCTTGGAGATGCCAGAGGGGACCCGCCAGAAAGCCAAAGACAG 2228
 Db 2221 AATCCCAATACCTACCTTGGAGATGCCAGAGGGGACCCGCCAGAAAGCCAAAGACAG 2280
 Oy 2229 CTTCCTTTTCTGTGTCAAAAGTTTATGTCACAGATCATCTGTGTGAGGAAGAGCCCAAT 2288
 Db 2281 CTTCCTTTTCTGTGTCAAAAGTTTATGTCACAGATCATCTGTGTGAGGAAGAGCCCAAT 2340
 Oy 2289 CCATATTTGAAAATTCAGTACAGCCAGGGAATTTCTGTGTGAAAACCTTCACAG 2348
 Db 2341 CCATATTTGAAAATTCAGTACAGCCAGGGAATTTCTGTGTGAAAACCTTCACAG 2400
 Oy 2349 CACACCAAGGAGGAAGTCTAAATGCGACCATGATGAGACCCCTGGGGCTCA 2402
 Db 2401 CACACCAAGGAGGAAGTCTAAATGCGACCATGATGAGACCCCTGGGGCTCA 2454
 RESULT 6
 AB083367
 ID AB083367 standard; cDNA; 2870 BP.
 XX
 AC AB083367;
 XX
 XX 20-JAN-2003 (first entry)
 DT
 XX
 DE Human NR10.6 splicing variant encoding cDNA seq ID NO:9.
 XX
 KW NR10: splicing variant; haematopoietic receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH
 FT
 FT CDS
 FT tag= a
 FT /product= "NR10.6"
 PN
 XX
 PD 03-OCT-2002.
 XX
 XX 22-MAR-2002; 2002WO-JP02769.
 PE
 XX 26-MAR-2001; 2001JP-0087298.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Maeda M, Yaguchi N, Hasegawa M;
 PI
 DR WPI: 2003-018925/01.
 DR P-PSDB: ABP54367.
 XX
 PT NR10 splicing variants of haematopoietic receptor proteins and encoded
 PT genes, applicable in searching haematopoietic factors and developing
 PT remedies for immunological and haematopoietic diseases
 XX
 PS Claim 1; Fig 13-15; 250pp; Japanese.
 CC
 CC The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (i) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietic receptor genes participate
 CC in in vivo immunomodulation and haematopoietic cell regulation, and in
 CC the search for haematopoietic factors capable of functionally binding
 CC to the receptors. The present sequence encodes the human NR10.6 protein
 CC from the present invention.

xx Sequence 2870 bp; 799 A; 667 C; 709 G; 695 T; 0 other;
SQ
Query Match 89.9%; Score 2160; DB 25; Length 2870;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 2252; Conservative 0; Mismatches 0; Indels 82; Gaps 1;
OY 69 CTGGAAATGTCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGAATGTCG 128
DB 1 CTGGAAATGTCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGAATGTCG 60
OY 129 CAAAACATTCCTCTCCACCACCTTCATGTGTTAACTGGGATGATGACCTGGCA 188
DB 61 CAAAACATTCCTCTCCACCACCTTCATGTGTTAACTGGGATGATGACCTGGCA 120
OY 189 CTGGAGATGTCCTCCCTCACTCTGCAGAAATTCAGCCCTGGAGAGCTCTGCCAGCTAG 248
DB 121 CTGGAGATGTCCTCCCTCACTCTGCAGAAATTCAGCCCTGGAGAGCTCTGCCAGCTAG 180
OY 249 AACATTCCTCTGCTACTACTATAGAAAAATTTAACTGCACCTGGAGTCCAGAAAG 308
DB 181 AACATTCCTCTGCTACTACTATAGAAAAATTTAACTGCACCTGGAGTCCAGAAAG 240
OY 309 GAAACCACTTATACCCAGTACAGAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGAT 368
DB 241 GAAACCACTTATACCCAGTACAGAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGAT 300
OY 369 AATTGTACAAACAATAGTTTACAAAGTGAATAATGCTGTGCTCTTTTTCCTTCCA 428
DB 301 AATTGTACAAACAATAGTTTACAAAGTGAATAATGCTGTGCTCTTTTTCCTTCCA 360
OY 429 AGAATTAACGATCCAGATATTAATACATTTGAGTGAAGCTGAATAATGAGATGTGTA 488
DB 361 AGAATTAACGATCCAGATATTAATACATTTGAGTGAAGCTGAATAATGAGATGTGTA 420
OY 489 ATTAATCTCATATGACACTACTGGAGATTAGAGAACTAGCGAAACTGAACCACTAG 548
DB 421 ATTAATCTCATATGACACTACTGGAGATTAGAGAACTAGCGAAACTGAACCACTAG 480
OY 549 ATTTCCGCTGGAACCAAGTTTGGGCAATCAAGCAATGATTTCAATGATGATGAAG 608
DB 481 ATTTCCGCTGGAACCAAGTTTGGGCAATCAAGCAATGATTTCAATGATGATGAAG 540
OY 609 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATATACACTCTCGATTCCAGACAGTCAAC 668
DB 541 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATATACACTCTCGATTCCAGACAGTCAAC 600
OY 669 AGTACACACTGATGAGAGTCACTTGCCTAAGAACCTTAAGGATAAAAACCAACGTAAC 728
DB 601 AGTACACACTGATGAGAGTCACTTGCCTAAGAACCTTAAGGATAAAAACCAACGTAAC 660
OY 729 AACCTCAGGGGCTGCAGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAG 788
DB 661 AACCTCAGGGGCTGCAGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAG 720
OY 789 GAGTCAAAAGTCTGAGTGAAGTGAAGCAAGAAAAAATGGAAATGACTGAGGAAGAACT 848
DB 721 GAGTCAAAAGTCTGAGTGAAGTGAAGCAAGAAAAAATGGAAATGACTGAGGAAGAACT 780
OY 849 CCATGTGGCTGGAACTGTGAGAGTCTGAAACCAAGCTGAGGGGATGAGAAAGGCCA 908
DB 781 CCATGTGGCTGGAACTGTGAGAGTCTGAAACCAAGCTGAGGGGATGAGAAAGGCCA 840
OY 909 GTGGCGTTGTTATGGAAGAAGCAAGAGAGCCGAGCTAGAGAAAAACCTTGGCTAG 968
DB 841 GTGGCGTTGTTATGGAAGAAGCAAGAGAGCCGAGCTAGAGAAAAACCTTGGCTAG 900
OY 969 AACATATGTAATATCCAGAAAGCAACTAATCTCACAGAAACATGAGACTACTATAC 1028
DB 901 AACATATGTAATATCCAGAAAGCAACTAATCTCACAGAAACATGAGACTACTATAC 960
OY 1029 CAGACGCTTGAATGATCTGAGGAGGAGAGAGCTTTGGGTGTCATGATTTCTTATAT 1088
DB 1029 CAGACGCTTGAATGATCTGAGGAGGAGAGAGCTTTGGGTGTCATGATTTCTTATAT 1088

DB 961 CAGCAGCTGTAACATGATCTGGAGGAGAGAGCTTTTGGGTGTCATGATTTCTTATAT 1020
OY 1089 TCTCTTGGGAGATGTCAGTGGCCACCTCGAGATTCACGATTAACAAGAAATCATTT 1148
DB 1021 TCTCTTGGGAGATGTCAGTGGCCACCTCGAGATTCACGATTAACAAGAAATCATTT 1080
OY 1149 CAGTGCATATGAGTCAATGACAGGCTTGGTCTGAGACACAGTACGATGAGTGAATGGCAA 1208
DB 1081 CAGTGCATATGAGTCAATGACAGGCTTGGTCTGAGACACAGTACGATGAGTGAATGGCAA 1140
OY 1209 AGCTCTGCTAGACGTGACACTTGGATGATTAATGTTTCCGATGTGAGCTACAG 1268
DB 1141 AGCTCTGCTAGACGTGACACTTGGATGATTAATGTTTCCGATGTGAGCTACAG 1200
OY 1269 CCCACACCCCTTCTGGGAATCTGTCTCAGGCCACGAACTGAGAGATCCACCAAGAT 1328
DB 1201 CCCACACCCCTTCTGGGAATCTGTCTCAGGCCACGAACTGAGAGATCCACCAAGAT 1260
OY 1329 AAATTTAAACCTTTCTGTGCTATACATCTCTGTATCCAAATGTTGCATGACAAAGTT 1388
DB 1261 AAATTTAAACCTTTCTGTGCTATACATCTCTGTATCCAAATGTTGCATGACAAAGTT 1320
OY 1389 GCGCAGCCATATTCATCTCAGGCTTATGCCAAAGAGCGTCCATCAGAAAGTCTGAG 1448
DB 1321 GCGCAGCCATATTCATCTCAGGCTTATGCCAAAGAGCGTCCATCAGAAAGTCTGAG 1380
OY 1449 ACCAAGGTGAGAACATTTGGCGTGAAGCGGTACAGATCAGATGAAGAAAGATTTCCAG 1508
DB 1381 ACCAAGGTGAGAACATTTGGCGTGAAGCGGTACAGATCAGATGAAGAAAGATTTCCAG 1440
OY 1509 AGTGAAGAAAGGATATCATCTGCACTACACATCTTTTACAAAGCTGAAGGTGAGAA 1568
DB 1441 AGTGAAGAAAGGATATCATCTGCACTACACATCTTTTACAAAGCTGAAGGTGAGAA 1500
OY 1569 GGATTTCCCAAGACATCATTCAGACATCTGAGATGAGCGGCTGAGATCCCTAACAAG 1628
DB 1501 GGATTTCCCAAGACATCATTCAGACATCTGAGATGAGCGGCTGAGATCCCTAACAAG 1560
OY 1629 AAGACCTCTTACATTTGTCAGTCAATGCGCCAGCACAGTGTGGGGGAACCAAGGAG 1688
DB 1561 AAGACCTCTTACATTTGTCAGTCAATGCGCCAGCACAGTGTGGGGGAACCAAGGAG 1620
OY 1689 AGCATTAATTTCAAGACATTCATTCAGTGTCTTTGAGATTTATCTCATTAATCTCTG 1748
DB 1621 AGCATTAATTTCAAGACATTCATTCAGTGTCTTTGAGATTTATCTCATTAATCTCTG 1680
OY 1749 ATTTGAGAGGCTTCTTATCTCATATATCTGACAGTGGCATGATGCTCAAAAACCC 1808
DB 1681 ATTTGAGAGGCTTCTTATCTCATATATCTGACAGTGGCATGATGCTCAAAAACCC 1740
OY 1809 AACAAATTTGACATCTGTGTGGCCCAACCTTCCCAACCTGCTGAAGTATAGCC 1868
DB 1741 AA----- 1742
OY 1869 ACATGCAATGAGATGATTTCAAGATTAAGTAAACCTGAAGAGTCTGATGACTGTG 1928
DB 1743 -----GATTAAGCTTAACCTGAAGAGTCTGATGATGACTGTG 1778
OY 1929 AACACAGAGACAGATCTTAAACCAATGTTCCACCCCGAGTGCAGATGGTGTATGAC 1988
DB 1779 AACACAGAGACAGATCTTAAACCAATGTTCCACCCCGAGTGCAGATGGTGTATGAC 1848
OY 1889 AAGTTGGTGGGAACTTGGGAATGTCTGCAAAATTTTTCACAGATGAAGCCAGAAC 2048
DB 1839 AAGTTGGTGGGAACTTGGGAATGTCTGCAAAATTTTTCACAGATGAAGCCAGAAC 1888
OY 2049 GGTGAGGAAACAAATTTAGAGGGGAAAGAAATGGATGTGACCTGCCCTTCAGGCT 2108
DB 1889 GGTGAGGAAACAAATTTAGAGGGGAAAGAAATGGATGTGACCTGCCCTTCAGGCT 1958
OY 2109 GATTTGCCCTGGGGAAGATTTTGGAGAGTCCCACTTTTACCTGAGATTTCCGCCAGA 2168
DB 1959 GATTTGCCCTGGGGAAGATTTTGGAGAGTCCCACTTTTACCTGAGATTTCCGCCAGA 2018


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D 1021 TCTCTGGGAAGTCTCCAGTGGCCACCCTGAGATTCCAGTATTCAGAAAAATCATTT 1080
O 1149 CAGTGCATTTGAGGTCATCAGCCCTGCTGTGAGCAGCATAGTGTGAAGTGGCAA 1208
D 1081 CAGTGCATTTGAGGTCATCAGCCCTGCTGTGAGCAGCATAGTGTGAAGTGGCAA 1140
O 1209 AGCTGTGCTAGAGTGAACACTTGTGATTTGATTTGATTTGATTTGATTTGATTTG 1268
D 1141 AGCTGTGCTAGAGTGAACACTTGTGATTTGATTTGATTTGATTTGATTTGATTTG 1200
O 1269 CCCACACCCCTTCTCTGGGATCTGTGCTCAGGCCACAGAACTGGAGCATCCAGAGAT 1328
D 1201 CCCACACCCCTTCTCTGGGATCTGTGCTCAGGCCACAGAACTGGAGCATCCAGAGAT 1260
O 1329 AAATTTAAACCTTCTGTGCTATACATCTGTGTATCCATGTTTCATGACAAAGTT 1388
D 1261 AAATTTAAACCTTCTGTGCTATACATCTGTGTATCCATGTTTCATGACAAAGTT 1320
O 1389 GCGGAGCCATATTCATCCATCAGGCTTATGCAAGAGGCGTTCCATCAGAAAGTCTGAG 1448
D 1321 GCGGAGCCATATTCATCCATCAGGCTTATGCAAGAGGCGTTCCATCAGAAAGTCTGAG 1380
O 1449 ACCAAGGTGAGACATTTGGGCTGAAGCGTCAAGCATCATGGAAGAGATTTCCAG 1508
D 1381 ACCAAGGTGAGACATTTGGGCTGAAGCGTCAAGCATCATGGAAGAGATTTCCAG 1440
O 1509 AGTGAAGAAAGGATCATCTGCAACATCTTTTACCAAGCTGAAGTGGAAAA 1568
D 1441 AGTGAAGAAAGGATCATCTGCAACATCTTTTACCAAGCTGAAGTGGAAAA 1500
O 1569 GGATTTCTCAAGACATCAATTCACGATCTTTCAGATGCGCTGAGAGTCCCTGAACGA 1628
D 1501 GGATTTCTCAAGACATCAATTCACGATCTTTCAGATGCGCTGAGAGTCCCTGAACGA 1560
O 1629 AAGACCTCTCATTTGTTCAGTGTGAGCGCAGACCATGCTGGGGGGAACCAAGGGAGC 1688
D 1561 AAGACCTCTCATTTGTTCAGTGTGAGCGCAGACCATGCTGGGGGGAACCAAGGGAGC 1620
O 1689 AGCATAAATTTCAAGACATTCATCAGTGTCTTTGAGATTATCCATTAACCTTCTGTG 1748
D 1621 AGCATAAATTTCAAGACATTCATCAGTGTCTTTGAGATTATCCATTAACCTTCTGTG 1647
O 1749 ATTGGTGGAGGCTTCTTATTCATTAATCTGACAGTGCATATGCTCAAAAAACC 1808
D 1648 ----- 1647
O 1809 AACAAATTCATCTGCTGTGTTGGCCACCGTCCCAACCTGCTGAAAGTATATACC 1868
D 1648 -ACAATTTGACTCATCTGTGTTGGCCACCGTCCCAACCTGCTGAAAGTATATACC 1706
O 1869 ACATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTGTGATGACTGTG 1928
D 1707 ACATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTGTGATGACTGTG 1766
O 1929 AACACAGAACAGAGATTTAAACCATGTTCCACCCCACTGACAAAGTGTGATTTGAC 1988
D 1767 AACACAGAACAGAGATTTAAACCATGTTCCACCCCACTGACAAAGTGTGATTTGAC 1826
O 1989 AAGTTGGTGGTGAATTTGGGAATGTTGCAAGAAATTTCAAGATGAGAGCCAGAACG 2048
D 1827 AAGTTGGTGGTGAATTTGGGAATGTTGCAAGAAATTTCAAGATGAGAGCCAGAACG 1886
O 2049 GGTGAGGAAAAATTTAGAGGGGAAAAAAGATGGTATGTGACCTGCGCCCTTACAGGCT 2108
D 1887 GGTGAGGAAAAATTTAGAGGGGAAAAAAGATGGTATGTGACCTGCGCCCTTACAGGCT 1946
O 2109 GATTTGCTCCCTGGGAAAAAGTTTGGAGAGTCCCAAGTTTCACTGAGATTTCCGCCAGA 2168
D 1947 GATTTGCTCCCTGGGAAAAAGTTTGGAGAGTCCCAAGTTTCACTGAGATTTCCGCCAGA 2006
O 2169 AAATCCCAATACCTACGTTGAGGATGCGACAGGGGAGCCGCCCAAGAACCAAGAGACAG 2228
D 2007 AAATCCCAATACCTACGTTGAGGATGCGACAGGGGAGCCGCCCAAGAACCAAGAGACAG 2066
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O 2229 CTCTCTTTTGTGTCAGAGTTTATGATCAGATCATCTGTGTGAGGAAGAGCCCAAT 2288
D 2067 CTCTCTTTTGTGTCAGAGTTTATGATCAGATCATCTGTGTGAGGAAGAGCCCAAT 2126
O 2289 CCATATTTGAAAAATTCAGTACGACAGCCAGGGAATTTCTGTGTGAAAAATTCAGAG 2348
D 2127 CCATATTTGAAAAATTCAGTACGACAGCCAGGGAATTTCTGTGTGAAAAATTCAGAG 2186
O 2349 CACACCAAGGAGAGTCTTAATGCGACCATAGCATGAGACCTCGGGGCTCA 2402
D 2187 CACACCAAGGAGAGTCTTAATGCGACCATAGCATGAGACCTCGGGGCTCA 2240

RESULT 8
ABA93803
ID ABA93803 standard; cDNA: 2529 BP.
XX
AC ABA93803;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17 cDNA sequence SEQ ID NO:45.
XX
KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antidiarrhetic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
OS Homo sapiens.
XX
PN WO20020721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujper JL;
PI Maurer MP;
XX
DR WI: 2002-090519/12.
XX
P-PSDB: ABB05738.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Claim 2; Page 190-194; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, antidiarrhetic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
```



```
RESULT 9
ID ABQ83363
ABQ83363 standard; cDNA: 4315 BP.
XX
AC ABQ83363;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.3 splicing variant encoding cDNA SEQ ID NO:1.
XX
KW NR10; splicing variant; haematopoietic receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2052
FT /tag= a
FT /product= "NR10.3"
XX
XX WO200277230-A1.
XX
XX 03-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-JP02769.
XX
XX 26-MAR-2001; 2001JP-0087298.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Maeda M, Yaguchi N, Hasegawa M;
XX
XX WPI: 2003-018925/01.
XX
XX P-PSDB: ABP54363.
XX
XX NR10 splicing variants of hematopoietic receptor proteins and encoded
XX genes, applicable in searching hematopoietic factors and developing
XX remedies for immunological and hematopoietic diseases
XX
XX Example 2; Fig 1-2; 250pp: Japanese.
XX
XX The present invention describes haematopoietic receptor NR10 splicing
XX variants (I). (i) have immunomodulator and haemostatic activities. The
XX proteins and encoded genes are applicable in searching for novel
XX haematopoietic factors, and developing remedies for immunological and
XX haematopoietic diseases. The haematopoietic receptor genes participate
XX in vivo immunomodulation and haematopoietic cell regulation, and in
XX the search for haematopoietic factors capable of functionally binding
XX to the receptors. The present sequence encodes the human NR10.3 protein
XX from the present invention.
XX
XX Sequence 4315 BP: 1187 A; 1008 C; 1061 G; 1059 T; 0 other;
XX
Query Match 83.9%; Score 2016; DB 25; Length 4315;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 CTGGGAATGTCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGTAATGCCG 128
DB 1 CTGGGAATGTCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGTAATGCCG 60
QY 129 CAAACATTCCTCTCCCGACCTTCATGTGTTAACTGGGAGTATGTGACCTGGGCA 188
DB 61 CAAACATTCCTCTCCCGACCTTCATGTGTTAACTGGGAGTATGTGACCTGGGCA 120
QY 189 CTGTGATGCTCCCGTCACTCTGCAAAATTAAGCTGGAGCTGGCCAGCTAAAGCTGAG 248
DB 121 CTGTGATGCTCCCGTCACTCTGCAAAATTAAGCTGGAGCTGGCCAGCTAAAGCTGAG 180
QY 249 AACATTTCTGTGTCTACTACTATATGAAAAATTTAACTGCACTTGAGTCCAGAAAG 308
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DB 181 AACATTTCTGTGTCTACTACTATATGAAAAATTTAACTGCACTTGAGTCCAGAAAG 240
QY 309 GAAACCGATTATACCCAGTACACAGTTTAAGAAACTTACGCTTTTGGAGAAAAACATGAT 368
DB 241 GAAACCGATTATACCCAGTACACAGTTTAAGAAACTTACGCTTTTGGAGAAAAACATGAT 300
QY 369 AATTGTACAAACCAATAGTCTTACAAAGTGAAGTGAAGTGTGCTGCTTTTTCCTTCCA 428
DB 301 AATTGTACAAACCAATAGTCTTACAAAGTGAAGTGAAGTGTGCTGCTTTTTCCTTCCA 360
QY 429 AGAATTAACGATCCAGATTAATTAATACATTGAGGTGAAGCTGAAAAATGAGATGTGTA 488
DB 361 AGAATTAACGATCCAGATTAATTAATACATTGAGGTGAAGCTGAAAAATGAGATGTGTA 420
QY 489 ATTAATTCATATAGCATACTGAGATTTAGAGAACATAGCGAAACTGAACCCCTAAG 548
DB 421 ATTAATTCATATAGCATACTGAGATTTAGAGAACATAGCGAAACTGAACCCCTAAG 480
QY 549 ATTTCCGTTGGAACACAGTTTGGGATCAAAACGAATGATTCAAATTTGAATGATTAAG 608
DB 481 ATTTCCGTTGGAACACAGTTTGGGATCAAAACGAATGATTCAAATTTGAATGATTAAG 540
QY 609 CTTGAGTTGGGCGCTGTTTCATCTGATTTAAATATACACACTTCGATTCAGGACAGTCAAC 668
DB 541 CTTGAGTTGGGCGCTGTTTCATCTGATTTAAATATACACACTTCGATTCAGGACAGTCAAC 600
QY 669 AGTACCAAGCTGATGGAAGTCACTTGGCTTAAGAACCTTAAGATTAATAAACCAAGCTAC 728
DB 601 AGTACCAAGCTGATGGAAGTCACTTGGCTTAAGAACCTTAAGATTAATAAACCAAGCTAC 660
QY 729 AACCTCACGGGGCTGCGACCTTTTACAGAAATATGTACTGCGATGCGGGTCAAG 788
DB 661 AACCTCACGGGGCTGCGACCTTTTACAGAAATATGTACTGCGATGCGGGTCAAG 720
QY 789 GAGTCAAAAGTCTGAGTGAAGTCACTGAGGCCAAGAAAAATGGAATGACTGAGAAAGACT 848
DB 721 GAGTCAAAAGTCTGAGTGAAGTCACTGAGGCCAAGAAAAATGGAATGACTGAGAAAGACT 780
QY 849 CCATGTGCGCTGGAACTGTGAGAGTCCGTAAGAACCACTGAGCGGATGGAAGAACGCCA 908
DB 781 CCATGTGCGCTGGAACTGTGAGAGTCCGTAAGAACCACTGAGCGGATGGAAGAACGCCA 840
QY 909 GTGGCGTTGTTATGGAAGCAAGGCAAGAGAGCCCACTCTAGAGAAACACTTGGCTAC 968
DB 841 GTGGCGTTGTTATGGAAGCAAGGCAAGAGAGCCCACTCTAGAGAAACACTTGGCTAC 900
QY 969 AACATATGTAATATCCAGAAAGCAACACTTACCTACAGAAACCAATGAACACTACTAAC 1028
DB 901 AACATATGTAATATCCAGAAAGCAACACTTACCTACAGAAACCAATGAACACTACTAAC 960
QY 1029 CAGCAGCTTGAACGATCTGAGGAGGAGGAGAGCTTTGGGTGCTATGATTTCTTAAT 1088
DB 961 CAGCAGCTTGAACGATCTGAGGAGGAGGAGAGCTTTGGGTGCTATGATTTCTTAAT 1020
QY 1089 TCTCTTGGGAAGTCTCAGTGGCCACCTCAGATTCACATTAATCAAGAAAAATCAATT 1148
DB 1021 TCTCTTGGGAAGTCTCAGTGGCCACCTCAGATTCACATTAATCAAGAAAAATCAATT 1080
QY 1149 CAGTCAATGAGTCAATGACAGGCGCTGCTGCTGAGAGCAGCTAGTGTGAAGTGGCAA 1208
DB 1081 CAGTCAATGAGTCAATGACAGGCGCTGCTGCTGAGAGCAGCTAGTGTGAAGTGGCAA 1140
QY 1209 AGCTCTGCTCTAAGACGTGAACACTTGTGATTAATGATTTCCGAGTGTGACCTCAGAG 1268
DB 1141 AGCTCTGCTCTAAGACGTGAACACTTGTGATTAATGATTTCCGAGTGTGACCTCAGAG 1200
QY 1269 CCCAGCACCTTTCCTGGAATCTGTCTCAGGCCAGAACTGGAGATCCGACAAAGAT 1328
DB 1201 CCCAGCACCTTTCCTGGAATCTGTCTCAGGCCAGAACTGGAGATCCGACAAAGAT 1260
QY 1329 AAATTAACCTTTCCTGCTATACATCTGTGTATCAATGTTGATGATGACAAAGTT 1388
DB 1329 AAATTAACCTTTCCTGCTATACATCTGTGTATCAATGTTGATGATGACAAAGTT 1388
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Dp	1261	AAATTAACACCTTTCTGCTCTATACATCTCTGTGTATCCAAATGTTGCATGACAAAGTT	1320
Qy	1389	GGCGAGCCAAATTCATCCAGGCTTATGCCAAGAAGGCGTTCATCAGAGGCTCGAG	1448
Dp	1321	GGGAGGCAATTCATCCAGGCTTATGCCAAGAAGGCGTTCATCAGAGGCTCGAG	1380
Qy	1449	ACCAAGGTGAGAACATTTGGCGTGAAAGCGGTACGATCAATGAAAAGATTTCCCAAG	1508
Dp	1381	ACCAAGGTGAGAACATTTGGCGTGAAAGCGGTACGATCAATGAAAAGATTTCCCAAG	1440
Qy	1509	AGTGAAGAAAAGGTTATCATCTGCACTACACCATCTTTTACCAGACTGAAGGTGAAAA	1568
Dp	1441	AGTGAAGAAAAGGTTATCATCTGCACTACACCATCTTTTACCAGACTGAAGGTGAAAA	1500
Qy	1569	GGATTCCTCCAAAGACAGTCAATTCACAGATCTTGGAGTACGGCGTGGAGTCCCTGAACGA	1628
Dp	1501	GGATTCCTCCAAAGACAGTCAATTCACAGATCTTGGAGTACGGCGTGGAGTCCCTGAACGA	1560
Qy	1629	AAGACCTCTTACATTTGTTCAAGTTCATGGCCAGCACACAGTCTGGGGGAACCAAGGGACC	1688
Dp	1561	AAGACCTCTTACATTTGTTCAAGTTCATGGCCAGCACACAGTCTGGGGGAACCAAGGGACC	1620
Qy	1689	AGCATTAATTTCAAGACATTTGTCTATTAAGTGTCTTTAGATTAATTCCTATTAATCTCTGTG	1748
Dp	1621	AGCATTAATTTCAAGACATTTGTCTATTAAGTGTCTTTAGATTAATTCCTATTAATCTCTGTG	1680
Qy	1749	ATTGTTGGAGGCGCTCTTATTTCTATTCATATTCCTGACATGGCATTTGGTCTCCAAAAAACC	1808
Dp	1681	ATTGTTGGAGGCGCTCTTATTTCTATTCATATTCCTGACATGGCATTTGGTCTCCAAAAAACC	1740
Qy	1809	AACAAATTTGACTCATCTGTGTGTCGCCACCGTTCGCCAACCTGCTGGAAGTAGTATAGCC	1868
Dp	1741	AACAAATTTGACTCATCTGTGTGTCGCCACCGTTCGCCAACCTGCTGGAAGTAGTATAGCC	1800
Qy	1869	ACATGCGATGAGATGATTTTCAGAGATTAAGCTTAACCTGAAAGAGTGTGATGACTCTGTG	1928
Dp	1801	ACATGCGATGAGATGATTTTCAGAGATTAAGCTTAACCTGAAAGAGTGTGATGACTCTGTG	1860
Qy	1929	AACACAGACAGACAGATCTTAAAAACATGTTCCACCCCGCAGTGCACAGTTGGTATTTGAC	1988
Dp	1861	AACACAGACAGACAGATCTTAAAAACATGTTCCACCCCGCAGTGCACAGTTGGTATTTGAC	1920
Qy	1989	AAGTTGTTGTTGAATTTGGGAAATGTTCTGCACAGAAATTTTCACAGATGAAGCCAGAACG	2048
Dp	1921	AAGTTGTTGTTGAATTTGGGAAATGTTCTGCACAGAAATTTTCACAGATGAAGCCAGAACG	1980
Qy	2049	GGTCAGGAAAACAATTTAGAGGGGAAAAAGATGGG	2084
Dp	1981	GGTCAGGAAAACAATTTAGAGGGGAAAAAGATGGG	2016

RESULT	10
ABQ83369	
ID	ABQ83369 standard; cDNA; 2776 BP.
XX	
AC	ABQ83369;
XX	
DT	20-JAN-2003 (first entry)
DE	Human NR10.8 splicing variant encoding CDNA SEQ ID NO:13.
XX	
KW	NR10: splicing variant; haematopoieticn receptor; immunomodulator; haemostatic; haematopoietic factor; immunological disease; haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	CDS
FT	7..1653
FT	/*tag= a
FT	/product= "NR10.8"
PN	
	MO200277230-A1.

03-OCT-2002.
22-MAR-2002; 2002WO-JP02769.
26-MAR-2001; 2001JP-0087298.
(CHUS) CHUGAI SEIYAKU KK.
Maeda M, Yaguchi N, Hasegawa M;
WPI: 2003-018925/01.
P-PDB; ABP54369.

NR10 splicing variants of hematopoietin receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PR remedies for immunological and hematopoietic diseases

Claim 1; Fig 19-21; 250pp; Japanese.

The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence encodes the human NR10.8 protein
CC from the present invention.

Sequence 2776 BP; 776 A; 646 C; 692 G; 662 T; 0 other;

Query Match	82.1%	Score 1972	DB 25	Length 2776
Best Local Similarity	92.5%	Pred. No. 0		
Matches 2158	Conservative	0	Mismatches	0
			Indels	176
			Gaps	1
QY	CTGGAAATGTGCATAGGCAACCTCAAGTTTTCACCAAGGCATGTGCTGTAATGTCG	128		
Db	1 CTGGAAATGTGCATAGGCAACCTCAAGTTTTCACCAAGGCATGTGCTGTAATGTCG	60		
QY	129 CAAACATTTCTCTCTCCAGCCTTCATGTGTTAACTGGGATGATGTGACCTGGGCA	188		
Db	61 CAAACATTTCTCTCTCCAGCCTTCATGTGTTAACTGGGATGATGTGACCTGGGCA	120		
QY	189 CTGTGGATGTCTCCCTCACTCTGCAAAATTCACGCTTGCGACACTCTCCACCTGAG	248		
Db	121 CTGTGGATGTCTCCCTCACTCTGCAAAATTCACGCTTGCGACACTCTCCACCTGAG	180		
QY	249 AACATTTCTGTGTCTACTACTATATGAGAAAATTTAACTGTGACTTGGAGTCCAGGAAG	308		
Db	181 AACATTTCTGTGTCTACTACTATATGAGAAAATTTAACTGTGACTTGGAGTCCAGGAAG	240		
QY	309 GAAACCACTTATACCAGTACACAGCTTAAGAGAACTCAAGCTTTTGGAGAAAACATGAT	368		
Db	241 GAAACCACTTATACCAGTACACAGCTTAAGAGAACTCAAGCTTTTGGAGAAAACATGAT	300		
QY	369 AATTGTACACCAATAGTCTTCAAGAGTGAAGTCTGCTGCTCTTTTCTTCTTCCA	428		
Db	301 AATTGTACACCAATAGTCTTCAAGAGTGAAGTCTGCTGCTCTTTTCTTCTTCCA	360		
QY	429 AGAATTAACGATCCGATTAATTAATACCATGTGAGTGGAAAGCTGAAAATGGAGATGGTGA	488		
Db	361 AGAATTAACGATCCGATTAATTAATACCATGTGAGTGGAAAGCTGAAAATGGAGATGGTGA	420		
QY	489 ATTAAATCTCATATGACATACTGAGAGTTAGAGACATATAGCAAAACTGAAACCTCAAG	548		
Db	421 ATTAAATCTCATATGACATACTGAGAGTTAGAGACATATAGCAAAACTGAAACCTCAAG	480		
QY	549 ATTTTCCTGTGAACCACTTTGGGCAATCAACGAATGATTTCAAAATGATGATGAAG	608		
Db	481 ATTTTCCTGTGAACCACTTTGGGCAATCAACGAATGATTTCAAAATGATGATGAAG	540		
QY	609 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATTCACACTGTGAGTTAGGCACTCAAC	668		

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Db      |||||
541     CCTGAGTTGGCGCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGCTCAAC 600
Oy      669   AGTACACAGCTGGATGAAGTCAACTGCTAGAACCCCTAAGGATTAACCAACCAAGCTAC 728
Db      601   AGTACACAGCTGGATGAAGTCAACTGCTAGAACCCCTAAGGATTAACCAACCAAGCTAC 660
Oy      729   AACCTCAGCGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTCGGTCAAG 788
Db      661   AACCTCAGCGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTCGGTCAAG 720
Oy      789   GAGTAAAGTTCTGAGAGTACTGGAGCCAGAAAAAATGGGAATGACTGAGAGAGAGCT 848
Db      721   GAGTAAAGTTCTGAGAGTACTGGAGCCAGAAAAAATGGGAATGACTGAGAGAGAGCT 780
Oy      849   CCATGTGCGCTGGAACCTGTGAGAGTCTGAAACCAGCTGAGGGCGGATGGAAGAGGCA 908
Db      781   CCATGTGCGCTGGAACCTGTGAGAGTCTGAAACCAGCTGAGGGCGGATGGAAGAGGCA 840
Oy      909   GTGCGGTTGTTATGGAAGAGCAAGAGAGAGCCCGAGTCTAGAGAAAAACACTTGGCTAC 968
Db      841   GTGCGGTTGTTATGGAAGAGCAAGAGAGAGCCCGAGTCTAGAGAAAAACACTTGGCTAC 900
Oy      969   AACATATGCTACTATCCAGAAAGCAACCTAACCTCAGAGAAACATAGACTACTAAC 1028
Db      901   AACATATGCTACTATCCAGAAAGCAACCTAACCTCAGAGAAACATAGACTACTAAC 960
Oy      1029  CAGCAGCTTGAACCTGATCTGAGGAGCGAGAGCTTTGGGTGTCATGATTTCTATATAT 1088
Db      961   CAGCAGCTTGAACCTGATCTGAGGAGCGAGAGCTTTGGGTGTCATGATTTCTATATAT 1020
Oy      1089  TCTCTTGGGAAAGTCTCCAGTGGCCACCCCTGAGAGATTCAGAGTATTCAGAAAAATCATTT 1148
Db      1021  TCTCTTGGGAAAGTCTCCAGTGGCCACCCCTGAGAGATTCAGAGTATTCAGAAAAATCATTT 1080
Oy      1149  CAGTGCATGAGGATCATCAGAGCCCTGGCTGCTGAGGACAGCTAGTGTGTAAGTGGCAA 1208
Db      1081  CAGTGCATGAGGATCATCAGAGCCCTGGCTGCTGAGGACAGCTAGTGTGTAAGTGGCAA 1140
Oy      1209  AGCTCTGCTTAGACGTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
Db      1141  AGCTCTGCTTAGACGTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Oy      1269  CCCACACACCTTTTCTGCGGAATCTGTGTCAGAGCCACAGAACTGGAGCATCCAGCAAGAT 1328
Db      1201  CCCACACACCTTTTCTGCGGAATCTGTGTCAGAGCCACAGAACTGGAGCATCCAGCAAGAT 1260
Oy      1329  AAATTTAAACCTTCTGCTGCTATACATCTGCTGATTCATGCAATGTTGCATGACAAAGTT 1388
Db      1261  AAATTTAAACCTTCTGCTGCTATACATCTGCTGATTCATGCAATGTTGCATGACAAAGTT 1320
Oy      1389  GGGCAGCCATATTCATCCAGGCTTATGCAAGAGAGCGTTCCATCAGAGATCCTGAG 1448
Db      1321  GGGCAGCCATATTCATCCAGGCTTATGCAAGAGAGCGTTCCATCAGAGATCCTGAG 1380
Oy      1449  ACCAAGGTGGAGAACATTTGGCGTGAAGCGTCAAGGATCACAATGGAAGAGATTCCTCAAG 1508
Db      1381  ACCAAGGTGGAGAACATTTGGCGTGAAGCGTCAAGGATCACAATGGAAGAGATTCCTCAAG 1440
Oy      1509  AGTGAGAAAGGGGATCATCTGCAACATACACATCTTTTCCCAAGCTGGAAGGTGGAAAA 1568
Db      1441  AGTGAGAAAGGGGATCATCTGCAACATACACATCTTTTCCCAAGCTGGAAGGTGGAAAA 1500
Oy      1569  GGATTTCTCAAGACAGTCAATTCAGATCTTTCAGATACGGCCCTGAGATCCTTCAACGA 1628
Db      1501  GGATTTCTCAAGACAGTCAATTCAGATCTTTCAGATACGGCCCTGAGATCCTTCAACGA 1560
Oy      1629  AAGACCTCTTACATTTGTCAGGTCATGGCCAGCACCACTGCTGGGGGCAACCAAGGGGACC 1688
Db      1561  AAGACCTCTTACATTTGTCAGGTCATGGCCAGCACCACTGCTGGGGGCAACCAAGGGGACC 1620
Oy      1689  AGCATAAATTTCAAGACATTTGTCAGGTCCTTTGAGATTATCCTCATTAACCTTCTCTG 1748

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Db      1621  AGCATAAATTTCAAGACATTCATCTCA----- 1648
Oy      1749  ATGTGAGAGGCTCTTATTCATCTATATCTGACAGTGGCATATGCTCAAAAAAACCC 1808
Db      1649  ----- 1648
Oy      1809  AACAAATTGACTCATCTGTGTGGCCACCGCTTCCCAACCCCTGCTGAAGATGATATACCC 1868
Db      1649  ----- 1648
Oy      1869  ACATGGCATGGAGATGATTTAAGGATATAGCTAAACCTGGAAGAGCTGTGATGACTCTGTG 1928
Db      1649  -----GATTAAGCTAAACCTGGAAGAGTGTGATGACTCTGTG 1684
Oy      1929  AACACAGAAGCAGAGATCTTAAACCATGTTCCACCCCGACCTGACCAATGTTGGTATAC 1988
Db      1685  AACACAGAAGCAGAGATCTTAAACCATGTTCCACCCCGACCTGACCAATGTTGGTATAC 1744
Oy      1989  AAGTTGGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACG 2048
Db      1745  AAGTTGGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACG 1804
Oy      2049  GGTCAAGAAAAAATTTAGAGAGGGGAAAAAGATGGGTATGTGACCTGCCCCCTCAGGCTT 2108
Db      1805  GGTCAAGAAAAAATTTAGAGAGGGGAAAAAGATGGGTATGTGACCTGCCCCCTCAGGCTT 1864
Oy      2109  GATTGTCCCTGGGGGAAAGTTTGGAGAGCTCCAGTTCCAGCTGAGATTCGCCGCCGAGA 2168
Db      1865  GATTGTCCCTGGGGGAAAGTTTGGAGAGCTCCAGTTCCAGCTGAGATTCGCCGCCGAGA 1924
Oy      2169  AAATCCCAATACCTTTCAGAGATGTCAGAGGGGACCCGCCAGAAAGCCAAAGAGAGAG 2228
Db      1925  AAATCCCAATACCTTTCAGAGATGTCAGAGGGGACCCGCCAGAAAGCCAAAGAGAGAG 1984
Oy      2229  CTCTCTTTTCTGCTGCAAGATTTAGTACCAATCATCTGTGTGAGGAAGAGCCCAAT 2288
Db      1985  CTCTCTTTTCTGCTGCAAGATTTAGTACCAATCATCTGTGTGAGGAAGAGCCCAAT 2044
Oy      2289  CCATATTTGAAAAAATTCAGTACAGAGCCAGGAATTTCTGTCTGGAAGAACTTCAGAG 2348
Db      2045  CCATATTTGAAAAAATTCAGTACAGAGCCAGGAATTTCTGTGTCTGGAAGAACTTCAGAG 2104
Oy      2349  CACACCAAGGAGAGATCTAATAGCGACCATAGCATAGAGACCTCGGGGGCTCTCA 2402
Db      2105  CACACCAAGGAGAGATCTAATAGCGACCATAGCATAGAGACCTCGGGGGCTCTCA 2158

RESULT 11
AC92350
ID AC92350 standard; cdna: 2119 BP.
XX
AC92350;
XX
AC 26-MAR-2001 (first entry)
XX
DE Human haemopoietin receptor protein NR10.3 encoding cdna seq ID NO:16.
XX
KW Human: haemopoietin receptor: NR10.1; NR10.2; NR10.3; NR10:
XX immunoregulation; haematopoietic cell regulation; transmembrane;
XX immune disorder; haematopoietic disorder; autoimmune disease; allergy;
XX metal allergy; pollen allergy; ss.
XX Homo sapiens.
XX OS
XX PN WO200075314-A1.
XX PD 14-DEC-2000.
XX PF 01-JUN-2000; 2000WO-JP03556.
XX PR 02-JUN-1999; 99JP-0155797.
XX PR 30-JUL-1999; 99JP-0217797.
XX

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Db 1757 GGAGATGATTCAAGATAAGCTAAACCTGAAGAGTGTGATGACTGTGTGAACACAGAA 1816
QY 1938 GACAGATCTTAAACCATGTTCCACCCCACTGCACTGCTGATGACAGATTGGTG 1997
Db 1817 GACAGATCTTAAACCATGTTCCACCCCACTGCACTGCTGATGACAGATTGGTG 1876
QY 1998 GTGAACCTTGGGAATGTTCTGCAGAGAAATTTTCACAGATGAAGCAGACGGTCCAGAA 2057
Db 1877 GTGAACCTTGGGAATGTTCTGCAGAGAAATTTTCACAGATGAAGCAGACGGTCCAGAA 1936
QY 2058 AACCAATTTAGAGGGGAGAAAGATGGG 2084
Db 1937 AACCAATTTAGAGGGGAGAAAGATGGG 1963
RESULT 12
ABA93808
ID ABA93808 standard; cDNA: 2903 BP.
XX
AC ABA93808;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17 cDNA sequence SEQ ID NO:53.
XX
KM zcytor17: chromosome 5: 5q11: cytokine receptor; immunomodulatory;
KM antiinflammatory; antiviral; antirheumatic; ankylosing; cytostatic;
KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
OS Homo sapiens.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PE 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;
PI Mauder WF;
XX
DR WPI: 2002-090519/12.
DR P-PSDB; ABB05741.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Example 1: Page 199-203; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, ankylosing and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to

CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 other:
Query Match 81.0%; Score 1945.4; DB 24; Length 2903;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1946; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 138 CTCTTCCCAAGCCTTTCATGTTTAACTGGGAGATGATGAGCTGGGCACTGTGATG 197
Db 503 CTCTTCCCAAGCCTTTCATGTTTAACTGGGAGATGATGAGCTGGGCACTGTGATG 562
QY 198 CTCTTCCCAAGCCTTTCATGTTTAACTGGGAGATGATGAGCTGGGCACTGTGATG 257
Db 563 CTCTTCCCAAGCCTTTCATGTTTAACTGGGAGATGATGAGCTGGGCACTGTGATG 622
QY 258 TGTGTCTACTACTATAGGAAATTTAACTGCTGAGTCCAGAAAGAAACAGT 317
Db 623 TGTGTCTACTACTATAGGAAATTTAACTGCTGAGTCCAGAAAGAAACAGT 682
QY 318 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAATTGACA 377
Db 683 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAATTGACA 742
QY 378 ACCAATAGTCTACAAAGTAAATGCTGCTGCTCTTTTCTCCCAAGATTAACG 437
Db 743 ACCAATAGTCTACAAAGTAAATGCTGCTGCTCTTTTCTCCCAAGATTAACG 802
QY 438 ATCCCAATTAATTATACCATTTAGGTGAGTGAAGCTGAAATGAGATGTTAATTAATCT 497
Db 803 ATCCCAATTAATTATACCATTTAGGTGAGTGAAGCTGAAATGAGATGTTAATTAATCT 862
QY 498 CATATGACATCTGAGAGTTAGAGAACTAGCGAAACCTGAACCTTAAGTTTCCGT 557
Db 863 CATATGACATCTGAGAGTTAGAGAACTAGCGAAACCTGAACCTTAAGTTTCCGT 922
QY 558 GTGAACCAAGTTTGGGATCAAAACGATGATTTCAATTTGAATGATTAAGCTGAGTTG 617
Db 923 GTGAACCAAGTTTGGGATCAAAACGATGATTTCAATTTGAATGATTAAGCTGAGTTG 982
QY 618 GCGCCTGTTTCATGATTTAAATATACACACTTGCATTCAGAGACAGTACAGTACAGC 677
Db 983 GCGCCTGTTTCATGATTTAAATATACACACTTGCATTCAGAGACAGTACAGTACAGC 1042
QY 678 TGGATGGAAGTCAACTTGGCTTAAGAACCGTAAAGATTAATAACCAAGCTACAACTCCAGC 737
Db 1043 TGGATGGAAGTCAACTTGGCTTAAGAACCGTAAAGATTAATAACCAAGCTACAACTCCAGC 1102
QY 738 GGGCTGCAGCCTTTTACAGAAATATGTCATAGCTGCGGATGCAAGAGCAAG 797
Db 1103 GGGCTGCAGCCTTTTACAGAAATATGTCATAGCTGCGGATGCAAGAGCAAG 1162
QY 798 TTCTGGAAGTCAAGTGGAGCCCAAGAAATGGAATGACTGAGGAAGAAAGCTCATGTGCGC 857
Db 1163 TTCTGGAAGTCAAGTGGAGCCCAAGAAATGGAATGACTGAGGAAGAAAGCTCATGTGCGC 1222
QY 858 CTGGAACCTGTGGAAGTCTCTAAGAACCAAGCTAGGCGGATGGAAGAAAGCCAGTGGGTTG 917
Db 1223 CTGGAACCTGTGGAAGTCTCTAAGAACCAAGCTAGGCGGATGGAAGAAAGCCAGTGGGTTG 1282
QY 918 TTATGGAAGAGCAAGAGAGCCCAAGTCTAGAGAAACACTTGGTACAAACATATAGG 977
Db 1283 TTATGGAAGAGCAAGAGAGCCCAAGTCTAGAGAAACACTTGGTACAAACATATAGG 1342
QY 978 TACTATCCAGAAACCACTAATCTCAGAGAAACATGAACTACTATACCAAGAGCTT 1037
Db 1343 TACTATCCAGAAACCACTAATCTCAGAGAAACATGAACTACTATACCAAGAGCTT 1402
QY 1038 GAATGCAATCTGGGAGGAGAGAGCTTTGGGTGCTATGATTTCTTATATTTCTTGGG 1097
Db 1403 GAATGCAATCTGGGAGGAGAGAGCTTTGGGTGCTATGATTTCTTATATTTCTTGGG 1462

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OY 1098 AAGTCTCAGTGGCCACCCCTGAGATTCAGCTATTCAGAAAAATCATTTTCAGTGCAT 1157
    |||
    |||
    |||
Db 1463 AAGTCTCAGTGGCCACCCCTGAGATTCAGCTATTCAGAAAAATCATTTTCAGTGCAT 1522
    |||
    |||
    |||
OY 1158 GAGGTATGAGGCGCTGCTGCTGAGAGACACCTAGTGTGTAAGTGGCAAGCTCTGCT 1217
    |||
    |||
    |||
Db 1523 GAGGTATGAGGCGCTGCTGCTGAGAGACACCTAGTGTGTAAGTGGCAAGCTCTGCT 1582
    |||
    |||
    |||
OY 1218 CTGAGAGTGAACACTTGGATGATGTAATGTTCCGGATGTGGAGCTCAGAGCCACCACC 1277
    |||
    |||
    |||
Db 1583 CTGAGAGTGAACACTTGGATGATGTAATGTTCCGGATGTGGAGCTCAGAGCCACCACC 1642
    |||
    |||
    |||
OY 1278 CTTTCTGGGAATCTGTCTCAGGCCACGAACTGACATCCAGCAAGATTAATTAATA 1337
    |||
    |||
    |||
Db 1643 CTTTCTGGGAATCTGTCTCAGGCCACGAACTGACATCCAGCAAGATTAATTAATA 1702
    |||
    |||
    |||
OY 1338 CTTTCTGGGTCTATACATCTCTGTGTATCCAAATGTGTGATACAAAGTTGGCGAGCCA 1397
    |||
    |||
    |||
Db 1703 CTTTCTGGGTCTATACATCTCTGTGTATCCAAATGTGTGATACAAAGTTGGCGAGCCA 1762
    |||
    |||
    |||
OY 1398 TATTCCATCCAGGCTTATGCGCAAGAGGCGTTCATCAGAGGTCTCTGAGACCAAGTG 1457
    |||
    |||
    |||
Db 1763 TATTCCATCCAGGCTTATGCGCAAGAGGCGTTCATCAGAGGTCTCTGAGACCAAGTG 1822
    |||
    |||
    |||
OY 1458 GAGACATTTGGCGTGAAGACGCTCAGCATCATGGAAGAGATTCCCAAGAGTGAAGAGA 1517
    |||
    |||
    |||
Db 1823 GAGACATTTGGCGTGAAGACGCTCAGCATCATGGAAGAGATTCCCAAGAGTGAAGAGA 1882
    |||
    |||
    |||
OY 1518 AAGGTATCATCTGCAACTACACATCTTTTACCAGCTGAAGTGAAGAAAGATTTCTCC 1577
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    |||
    |||
Db 1883 AAGGTATCATCTGCAACTACACATCTTTTACCAGCTGAAGTGAAGAAAGATTTCTCC 1942
    |||
    |||
    |||
OY 1578 AAGACATCAATTCACAGCATCTTGACAGTACGGCTGGAGTCCCTGAAACGAAGACCTCT 1637
    |||
    |||
    |||
Db 1943 AAGACATCAATTCACAGCATCTTGACAGTACGGCTGGAGTCCCTGAAACGAAGACCTCT 2002
    |||
    |||
    |||
OY 1638 TACATTTGTCAGTGCATGCGCACGACCAAGTCTGGGGGGAACCAACGGGACACATTAAT 1697
    |||
    |||
    |||
Db 2003 TACATTTGTCAGTGCATGCGCACGACCAAGTCTGGGGGGAACCAACGGGACACATTAAT 2062
    |||
    |||
    |||
OY 1698 TTGAAGACATTTGTCATCTGCTTTGAGATTAATCTCTTAACCTCTCTGATTTGGTGA 1757
    |||
    |||
    |||
Db 2063 TTGAAGACATTTGTCATCTGCTTTGAGATTAATCTCTTAACCTCTCTGATTTGGTGA 2122
    |||
    |||
    |||
OY 1758 GGCCTTCTTATCTCATTTATCTGACAGTGGCATATGCTCAAAAACCAACCAATTTG 1817
    |||
    |||
    |||
Db 2123 GGCCTTCTTATCTCATTTATCTGACAGTGGCATATGCTCAAAAACCAACCAATTTG 2182
    |||
    |||
    |||
OY 1818 ACTCATCTGTGTGGGCCACCGTTCCCAACCTGCTGAAGATGATAGCCACATGGCAT 1877
    |||
    |||
    |||
Db 2183 ACTCATCTGTGTGGGCCACCGTTCCCAACCTGCTGAAGATGATAGCCACATGGCAT 2242
    |||
    |||
    |||
OY 1878 GAGATGATTTTCAAGATTAAGCTAAACCTGAAGAGTCTATGATCTGTGAACACAGAA 1937
    |||
    |||
    |||
Db 2243 GAGATGATTTTCAAGATTAAGCTAAACCTGAAGAGTCTATGATCTGTGAACACAGAA 2302
    |||
    |||
    |||
OY 1938 GACAGATCTTAAACCATGTTCCACCCCGAGTGAACAGTTGGATTTGAAGTTGGTG 1997
    |||
    |||
    |||
Db 2303 GACAGATCTTAAACCATGTTCCACCCCGAGTGAACAGTTGGATTTGAAGTTGGTG 2362
    |||
    |||
    |||
OY 1998 GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAAAGGCTCAGAA 2057
    |||
    |||
    |||
Db 2363 GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAAAGGCTCAGAA 2122
    |||
    |||
    |||
OY 2058 AACAAATTTAGAGGAGGAAAAAGATGGG 2084
    |||
    |||
    |||
Db 2423 AACAAATTTAGAGGAGGAAAAAGATGGG 2449
    |||
    |||
    |||

```

RESULT 13
 AAC92337
 ID AAC92337 standard: cDNA; 2969 BP.
 XX

```

AC AAC92337;
XX
XX 26-MAR-2001 (first entry)
DE Human haemopoietin receptor protein NR10.1 encoding cDNA SEQ ID NO:1.
XX
XX Human haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
XX immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy; ss.
XX
OS Homo sapiens.
XX
XX MO200075314-AL.
XX
XX 14-Dec-2000.
XX
XX 01-JUN-2000; 2000WO-JP03556.
XX
XX 02-JUN-1999; 99JP-0155797.
XX
XX 30-JUL-1999; 99JP-0217797.
XX
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Maeda M, Yaguchi N;
XX
XX WPI: 2001-061720/07.
XX
XX P-PSDB: AAB51242.
XX
XX Hematopoietin receptor protein NR10 for screening potential ligands for
XX treatment of immune and hematopoietic disorders such as autoimmune
XX diseases and allergies
XX
XX Claim 1; Fig 3-5; 127pp; Japanese.
XX
XX
XX The present sequence encodes a human haemopoietin receptor protein
XX (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
XX protein and a soluble protein. NR10 is a haemopoietin receptor molecule
XX which participates in immunoregulation and haematopoietic cell
XX regulation in vivo, and is useful in searching for haematopoietic
XX factors capable of binding to the receptor. NR10 can be used for the
XX identification of substances for the treatment and prevention of immune
XX and haematopoietic disorders including autoimmune diseases and allergies
XX such as metal and pollen allergy.
XX
XX Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 other;
XX
XX
XX Query Match 80.5%; Score 1932.8; DB 22; Length 2969;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1945; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
OY 138 CTCTCTCCCGAGGCTTCATGTGTTAACTGCGGATGATGTGGACCTGGGACATGTGGATG 197
    |||
    |||
    |||
Db 529 CTCTCTCCCGAGGCTTCATGTGTTAACTGCGGATGATGTGGACCTGGGACATGTGGATG 588
    |||
    |||
    |||
OY 198 CTCCCGTCACTGCAAAATTCAGCTGGGAGCTGCGACCTGAAGCTGGAACATTTTCC 257
    |||
    |||
    |||
Db 589 CTCCCGTCACTGCAAAATTCAGCTGGGAGCTGCGACCTGAAGCTGGAACATTTTCC 648
    |||
    |||
    |||
OY 258 TGTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGAGAAAGAACCACT 317
    |||
    |||
    |||
Db 649 TGTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGAGAAAGAACCACT 708
    |||
    |||
    |||
OY 318 TATACCCAGTACACAGCTTAAGAGAACTTACGCTTTTGGAGAAAAACATGTAATTTGACA 377
    |||
    |||
    |||
Db 709 TATACCCAGTACACAGCTTAAGAGAACTTACGCTTTTGGAGAAAAACATGTAATTTGACA 768
    |||
    |||
    |||
OY 378 ACCAATAGTCTCAAGTGAATAATCGTGTGCTCTTTTCCCTCCAGAAATTAAG 437
    |||
    |||
    |||
Db 769 ACCAATAGTCTCAAGTGAATAATCGTGTGCTCTTTTCCCTCCAGAAATTAAG 828
    |||
    |||
    |||
OY 438 ATCCAGATTAATTAACCATTTGAGGTGAAGCTGAATAATGAGATGATTAATTAATCT 497
    |||
    |||
    |||

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Oy	1911	GAGTCGTATGACTCTGTGGAAACACAGGAAGACAGAGATTCTTAAAACCATTGTTCCACCCCAGT	1970
Dd	1741	GARMSNGAYGSWNSGNTHAALPACAGARGAVYMGNTHTHNAARCCNTEGWSMACCKMWSN	1800
Oy	1971	GACAAGTTGGAGATTGACAAAGTTGGTGSGTGAACTTTGGGAATGTCTGCAGAAGAAATTTTC	2030
Dd	1801	GAYAAATYTNGINAHGAAVAAARYTMGTINCTNNAAYYTTYGSMALYGTINTINCARGAATAHTTY	1860
Oy	2031	ACAGATGAAGCCAGCAACGGGTCCAGAAAAACATTTAGAGGGGAAAAAGATGGTATGTG	2090
Dd	1861	ACONAYGARGCNMGNACNGNCACAGAAABAAAYAYTYNGNCGNGBARAAAYAGCATTAAGTN	1920
Oy	2091	ACCTGCCCCCTCAGAGCCTGATTGTCGCCCTGGGGAAAAAGTTTGGAGAGCTCCCGATTTC	2150
Dd	1921	ACNTGYCCNTTYMGNCNCGATYTTCYANTINGNMAARBSNTTYYGARGARITYTCCNGTWMSN	1980
Oy	2151	CCTGAGATTCCGCCAGAAAAATCCCAATACCTCACTCGAGATGCCAGAGGGGACCCGC	2210
Dd	1981	CCNGARATHCCNCCNMGMNAARWSNCARTAYTYTNMGNNMSNMGNANATGCCNGARGAACNMGN	2040
Oy	2211	CCAGAGGCCAAAGAGACGCTCTCTTTTCGTGCGTCAAAGTTTAGTACCAAGATCANCTGTGT	2270
Dd	2041	CCNGARGNMAARGARCARTYNTYTTTTWSNNGNCARBSNTYTNCCNGAICAYTYTNIGY	2100
Oy	2271	GAGGAGAGAGCCCCCAATTCATATTTTGAAAAATTCAGTACAGCCAGGAGATTTCTTGTC	2330
Dd	2101	GARGARGGNGCNCMAAYCCNTAYTYTNARAAYMSNTNMCNCGMONGARTYYTYNGTN	2160
Oy	2331	TCTGAAAAACTTCCAGAGCACACCAAGGGAGAGT	2365
Dd	2161	WSNGARAAARYTNCNGARCAVACNAARGANGRGRT	2195

XX	AB93821
XX	AB93821 standard; cDNA; 2295 BP.
XX	AB93821;
DT	01-MAY-2002 (first entry)
DE	Human zcytor17-Fc4 fusion polynucleotide SEQ ID NO:68.
KW	zcytor17; chromosome 5; Sgll; cytokine receptor; immunomodulatory;
KW	antiflammatory; antiviral; antirheumatic; antiarthritis; cyostatic;
KW	mucular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX	inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
OS	Homo sapiens.
OS	Synthetic.
PN	WO200200721-A2.
PD	03-JAN-2002.
PF	26-JUN-2001; 2001MO-US20484.
PR	26-JUN-2000; 2000US-214282P.
PR	29-JUN-2000; 2000US-214955P.
PR	08-FEB-2001; 2001US-267963P.
PA	(ZYMO) ZYMOGENETICS INC.
PI	Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kulper JL;
PI	Maurer MF;
DR	WPt: 2002-090519/12.
DR	P-PSDB: ABB05743.
XX	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is

PT useful for treating and diagnosing lymphoid, immune, inflammatory
PT splenic, blood or bone disorders -
XX
PS Example 11: Page 216-221; 235pp; English.

CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antitumematic, antithalritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.

SQ Sequence 2295 BP; 659 A; 578 C; 565 G;.493 T; 0 other;

Query Match	66.1%	Score 1586.8	DB 24	Length 2295
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1588; Conservative	0	Mismatches	2	Indels 0; Gaps 0

138 CTCTCTCCCGAGCCTTCATGTGTTAACCTGGGATGATGTGGACCTGGGCACCTGTGGATG 197

Db 7 CTCTCTCCCGAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGCACTGTGGATG 66

198 CTCCTCACTCTGCAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGACATTTCC 257

Db 67 CTCCTTCACTCTGCAATTACAGCTTGGCAGCTTGGCAGCTAAGCCTGAGACATTTCC 126

258 TGTGCTACTATAGGAAATTTAACTGCACCTTGGAGTCCAGGAAGGAACCACT 317

Db 127 TGTGCTCTACTATAGGAAATTTAACCTGCACCTTGGAGTCCAGGAAGGAACCACT 186

318 TATACCAGTACACAGTTAAGAGAACTTACGCTTTGGAGAAACATGATTAATGTACA 377

Db 187 TATACCAGTACACAGTTAAGAGAACTTACGCTTTGGAGAAAAACATGATAATTGTACA 246

378 ACCAATAGTCTCTACAAGTGAATACTGCTTCCTCTTTTTCCTTCCAAGATAACG 437

Db 247 ACCAATAGTCTCTACAAGTGAATACTGCTTCGTCCTCTTTTTCCTTCCAGAATAACG 306

438 ATCCAGATAATTATACCATTTGAGGTGGAAGCTGAAATGGAGATGGTGAATTAATCT 497

Db 307 ATCCGATAATTATACCATTGAGGTGGAAGCTGAAATGGAGATGGTCTAATTAAATCT 366

498 CATATGACATACTGGAGATTAGAGACATAGCGAAACTGGAACCACTAAGATTTTCCGT 557

Db 367 CATATGACATACTGGAGATTAGAGACATAGCGAAACTGACACCACCTAAGATTTCGGT 426

QY 558 GTGAACCAAGTTTGGGCATCAACGAATGATCAATTGAATGGATAAGCCTGAGTTC 617

Db 427 GTGAACCACTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAGCCTGAGTTC 486

618 GCGCCTGTTTCATCTGATTAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGC 677

Db 487 GCGCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGC 546

678 TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAACCAACGTACAACTCAG 737

Db 547 TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAACCAACGTACACCTCAG 606

738 GGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGAGTCAAC 797

Db 607 GGGCTGCAGCCTTTTACAGATATGTCATTAGCTCTGCATGTGGGTCAGGAGTCAAG 666

798 TTTCTGGAGTGA
CTGGAGCCAGA
AAAAATGGGA
TGA CTGAGGA
GAGCTCCATGT
GCC 857

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OM nucleic - nucleic search, using 'sw model

Run on: August 4, 2003, 18:18:26 ; Search time 141 Seconds

(without alignments)
7519.165 Million cell updates/sec

Title: US-09-892-949-1

Perfect score: 2402
Sequence: 1 ggcacagatgtgtgtgcag.....atgagacccctgggacctca 2402

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96.6	4.0	2369	1	US-07-797-556-1 Sequence 1, Appli
2	96.6	4.0	2369	1	US-08-308-881-1 Sequence 1, Appli
3	96.6	4.0	2369	2	US-09-058-283-1 Sequence 1, Appli
4	96.6	4.0	2369	2	US-09-058-039-1 Sequence 1, Appli
5	96.6	4.0	2369	3	US-09-058-264-1 Sequence 1, Appli
6	96.6	4.0	2369	4	US-09-455-962-1 Sequence 1, Appli
7	96.6	4.0	2369	5	PCT-US95-06530-1 Sequence 1, Appli
8	96.6	4.0	2754	2	US-08-825-558-5 Sequence 5, Appli
9	96.6	4.0	2754	4	US-09-312-611-5 Sequence 5, Appli
10	96.6	4.0	3085	3	US-08-795-473B-4 Sequence 4, Appli
11	96.6	4.0	3085	4	US-09-433-856-4 Sequence 4, Appli
12	76.4	3.2	1977	2	US-08-825-558-3 Sequence 3, Appli
13	76.4	3.2	1977	4	US-09-312-611-3 Sequence 3, Appli
14	76.4	3.2	3477	4	US-09-313-942-25 Sequence 25, Appli
15	76.4	3.2	3507	4	US-09-313-942-23 Sequence 23, Appli
16	75.4	3.1	2943	1	US-07-923-976-3 Sequence 3, Appli
17	75.4	3.1	3024	1	US-07-923-976-7 Sequence 7, Appli
18	74.4	3.1	3293	1	US-07-923-976-1 Sequence 1, Appli
19	69	2.9	2563	6	5422248-1 Patent No. 5422248
20	66	2.7	2855	1	US-07-923-976-5 Sequence 5, Appli
21	54.4	2.3	7218	1	US-08-232-463-14 Sequence 14, Appli
22	50.2	2.1	597	4	US-09-712-016-73 Sequence 73, Appli
23	44.2	1.8	3867	4	US-09-646-075-4 Sequence 4, Appli
24	37.2	1.5	3600	3	US-08-894-731-1 Sequence 1, Appli
25	36.4	1.5	12730	4	US-09-004-838-91 Sequence 91, Appli
26	36.4	1.5	12793	4	US-09-004-838-124 Sequence 124, App
27	36.4	1.5	15062	4	US-09-004-838-89 Sequence 89, Appli

28	35.4	1.5	580073	4	US-08-545-528D-1	Sequence 1, Appli
29	35	1.5	3312	4	US-09-669-751-259	Sequence 259, App
C 30	34.8	1.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
C 31	34.2	1.4	14602	1	US-08-597-236-1	Sequence 1, Appli
C 32	34.2	1.4	14602	1	US-08-746-682A-1	Sequence 1, Appli
C 33	34	1.4	2634	3	US-08-949-386-26	Sequence 26, Appli
C 34	34	1.4	2634	3	US-08-450-562-26	Sequence 26, Appli
C 35	34	1.4	2634	4	US-08-984-709A-26	Sequence 26, Appli
C 36	34	1.4	2634	4	US-08-450-272-26	Sequence 26, Appli
C 37	34	1.4	2712	3	US-08-949-386-38	Sequence 38, Appli
C 38	34	1.4	2712	3	US-08-450-562-38	Sequence 38, Appli
C 39	34	1.4	2712	4	US-08-984-709A-38	Sequence 38, Appli
C 40	34	1.4	2712	4	US-08-450-272-38	Sequence 38, Appli
C 41	34	1.4	2970	3	US-08-949-386-37	Sequence 37, Appli
C 42	34	1.4	2970	3	US-08-450-562-37	Sequence 37, Appli
C 43	34	1.4	2970	4	US-08-984-709A-37	Sequence 37, Appli
C 44	34	1.4	2970	4	US-08-450-272-37	Sequence 37, Appli
C 45	33.6	1.4	4223	3	US-09-541-782-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-07-797-556-1
Sequence 1, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Geating, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:

NAME/KEY: mat_peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 244..309
 US-07-797-556-1

Query Match 4.0%; Score 96.6; DB 1; Length 2369;
 Best Local Similarity 44.6%; Pred. No. 7.4e-20;
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

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OY 724 CGTACACCTCAGCGGGCTGCGCCTTTTACAGATATGTCACTCTGGAGTGGG 783
DB 1091 CATTACCTGTCCAAACCTTTAACTTTACAGATATGTGTTTGAAGATGCGTGTAGA 1150
OY 784 TCAAGAGTCAAG---TTTGGAGTGAAGAGCCAGCAAAAAATGGGAATGACTGAG 840
DB 1151 AGGAAGATGTGTAAGGATAGTGAAGTGAAGTGAAGCAAGTGGATCAGCTATG 1210.
OY 841 AAGAAGCTGCATGT---GGCCTGGAACCTGAGAGTCTCTGAACCACTGAGGGGATG 897
DB 1211 AAGATAGACCTTAAAGCCAGCTTTCTGTATATAATAGATCCATCCCTACTCAG 1270
OY 898 GAAGAAGGCCAGTGGGCTTTGTTATGAAGAAGCAAGAGAGCCAGTCCCTAGAGAAA 957
DB 1271 GCTACAGAACTGTACAACTCGTGTGAAGACATTTGCCCTTTTGAAGCCAAATGAAAA 1330
OY 958 CACTTGGCTACACATATGTACTATTCAGAAAGCAGACATTAACCTCAGAAACATGA 1017
DB 1331 TCTTGGATTATGAAGTGAAGTCTCAGAAAGATGAATACATTTTCAAAATTAACAGTTA 1390
OY 1018 ACACCTACTAACACAGAGCTTGAAGTCACTGTGGAGGAGAGAGCTTTGGTGTCTATGA 1077
DB 1391 ATGCCACAAACTGA-----CAGTAAATCTCACAAATAGATCGCTATGTACAAACCTTAA 1444
OY 1078 TTTCTTATATCTCTGTGGAGAGTCTCCAGTGGCCAGCCCTGAGAGATTCACATATCAAG 1137
DB 1445 CAGTAGAAATCTTTGGCAAAATCAGATGACAGCTGTTTAACTATCCCTGCTGAGCT 1504
OY 1138 AAAATCATTTTCAAGTCAATGAGGATGAGGAGGCTGGCTGTGAGAGACAGCTAGTGG 1197
DB 1505 TTCAAGCTACTACCCCTGTATGTGATCTTAAAGCATTCCTCCAAAGATTAACATGCTTTGGG 1564
OY 1198 TGAAGTGCAGAAAGCTCTGCTCTAGACGTGAACACTTGGATGATGAATGATTCGCGATG 1257
DB 1565 TGGATGAGTACTACTCAAGGAGATCTGTAAAGAAATATATCTTGAAGTGTGTGTAT 1624
OY 1258 TGGAGTGAAGCCAGCCAGCCCTTTCCGAGGATCTGTGTCTCAGGCCAGCACTGAGCA 1317
DB 1625 CAGATTAAGCACCCCTGTATCTACAGACTGGCAAGAAAGATGATGATGATGATGATGAT 1684
OY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGTATTAACATCTGTGTATCAATGTTGC 1377
DB 1685 ATTTAAGAGGAACTTGTAGAGAGCAAAATGCTTATTTGATTAACAGTACTCAATATATG 1744
OY 1378 ATGACAAAGTTGGCGAGCATATTCATCCAGGCTTATGCCAAGAAAGGCGTTCCATGAG 1437
DB 1745 CTGATGAGCAAGAGGAGCCCTGAATCATTAAGGATCACTTAAACAGATCCACACTTCCA 1804
OY 1438 AAGTCTCTGAGACCAAGAGTGAAGCAATTTGGCGTGAAGAGGATGATCATCATCAAGAG 1497
DB 1805 AAGGAGCTACTGTTCGAGCAAAAAAAGTAGGAAAAAGCAAGCTGTTCAGATGGGACC 1864
OY 1498 AGATTCCCAAGAGTGAAGAAAGGATTCATCTGCAACTACACCATCTTTTACCAACCTG 1557
DB 1865 AACTTCTCTGTGATGTTCAGATGATTTATCAGAAATTTATCTATATTTTATATGAGCA 1924
OY 1558 AAGTGAAGAAAGATTTTCCAAAGCATCAATTCACAGATCTTGCAGTACGGCTGAGT 1617
DB 1925 TCATTGGAATGAAGAACTGTGTGATGATGATTTTCCACACAGAAATATACATTTGCTT 1984
OY 1618 CCCGTAAGCAAGAGACCTTACATTTGAGTCAATGAGTGCAGACAGTGTGGGGGAA 1677

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DB 1985 CTTTGACTAGTACACATTTGATACATGTAGCAATGGCAGCATACAGATGAGTGGGA 2044
OY 1678 CCACGGGAGCAGCATATAATTTCAAGACATGTGCTATTCAGTCTTTGAGATATCTCCA 1737
DB 2045 AGGATGGTCCAGAAATCTTTTACTACCCCAAGATTGCTCAAGAGAAATTTGAAGCCA 2104
OY 1738 TAACCTCTGATTTGGTGGAGCGCTTCTTATTCATATTCATACAGATGSCATATGCTC 1797
DB 2105 TAGTCGTGCTGTTTCTTCTTACATTTCTATTCAGACACTCTCTGGAGTGTCTGTCTGCT 2164
OY 1798 TCAAAAAAACCACAAATTTGATCTATCTGTGTGGCCAGCCGTTCCCAACCTGCTGAA 1857
DB 2165 TTAATTAAGCAGACCTTAATTAATAAACACATCTGCGCTTAATGTTTCAGATTCCTTCAAGA 2224
OY 1858 CTAGTATAGCCACATGG 1874
DB 2225 GTCATATTTGCCAGTGG 2241

```

RESULT 2

US-08-308-881-1

Sequence 1, Application US/08308881

Patent No. 5783672

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2369 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TISSUE TYPE: human placenta

IMMEDIATE SOURCE:

CLONE: B10G/PDC303

FEATURE:

NAME/KEY: CDS

LOCATION: 244..2369

FEATURE:

NAME/KEY: mat_peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig_peptide.
 LOCATION: 244..309
 US-08-881-1

Query Match 4.08; Score 96.6; DB 1; Length 2369;
 Best Local Similarity 44.68; Pred. No. 7.4e-20;
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

724 CGTACACCTCAGCGGCTCAGCCCTTTTACAGAAATGTATGTCATGCTCGATGTCGG 783
 1091 CATCTACTGTCCAGAGCTTAACCTTTTACAGAAATGTATGTCATGCTCGATGTCGG 1150
 784 TCAAGAGTCAAG---TTCTGGAGTACTGAGACCCAGAAAAAATGGATGCTAGAG 840
 1151 AGGAAGATGTGTTAAGGATGCTGAGTGAAGAGCAAGTGGGTCACCTATG 1210
 841 AAGAAGCTCCATGT---GGCCTGGAAGTGTGAGAGTCTGGAACAGCTGAGCGGATG 897
 1211 AAGATTAACCATCTTAAGCACAAGTTTCTGTATTAATATGATCCATCTCATAG 1270
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 958 CACTGGCTACACATATGTACTATCCAGAAAGCACTACCTACAGAAACAATGA 1017
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 1445 CAGTAAGAAATCTTGTGGCAAAATCAGATGAGCTGTTTAACATATCCCTGCTGACT 1504
 1138 AAAATATCTTCATGATGATGAGTTCATGCAAGCCTGCTGCTGAGAGACAGTATGG 1197
 1505 TTCAAGTACTCACCCTGTATATGATCTTAAAGCATTCCTCCAAAGATTAACATGCTTGGG 1564
 1198 TGAAGTGGCAAGCTGTCTGTAGACGTGAACACTTGATGATGAATGTTCCGGATG 1257
 1565 TGAATGAGTACTCTCCAGGAATCTGTAAAGAAATATATCTGAGTGGTGTAT 1624
 1258 TGAAGTGAAGCCGACACCTTTCTGGAATCTGTCTCAGGCGACGAATGAGCA 1317
 1625 CAGATTAAGCACCTGTATCAGACAGTGGCAACAAGAAATGATGATCGTGCATGCACT 1684
 1318 TCCAGCAAGATTAATTAACCTTTCTGCTCTAATCATCTCTGTATCAATGTTGC 1377
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 1378 ATGACAAAGTTGGGAGCATATTCATTCACAGCTTATGCAAGAGGCGTTCATCAG 1437
 1745 CTGATGAGACCGAGAGCCCTGAATCCATTAAGGCACTACCTTAAACAGCTCCACTTCCA 1804
 1438 AAGTCTCTGAGACCAAGGTGAGAACATTTGCGGTGAAGACGTCACATCATGGAAG 1497
 1805 AAGGACCTACTGTTGCGCAAAAAGAGGAAAGAGAGCTGTTTAAAGTGGGACC 1864
 1498 AGATTCCCAAGAGTGAAGAGAAAGGTATCATCTGCACACTACCATCTTTTACCAAGCTG 1557
 1865 AACTTCCTGTTGATGTTCAGATGATTAATCAGAAATATATATATTTTATGAACCA 1924
 1558 AAGGTGGAAGAGATTTCCAAAGACATTCATTCAGAGATTTCCAGTACGCGCTGAGT 1617
 1925 TCATTGGAAATGAACAGCTGTGATGTGATTTCTTCCACACAGAAATATCATTTGCT 1984
 1618 CCCTGAAGAGAAAGCTCTTACATTTGTCAGGTCATGCGCAGCAGCACTGCTGGGGAA 1677

1985 CTTTGACTAGTGAACATGTTGATAGTGTAGCAATGGCAGCATACACAGATGAAGTGGGA 2044
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 2045 AGGATGCTCAGAAATTCATCTTACTACCCCAAGATTGCTCAAGAGAAATGAAGCCA 2104
 1738 TAACCTCTGATTTGGTGGAGCCCTTCTTATTCATATCTGCACAGTGGCATATGTC 1797
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 1798 TCAAAAACCCCAAAATGACTCATCTGTGTGGCCACCCTGTCCTCCACCTGCTGAAA 1857
 2165 TTAATAGCAGACCTTAATTAACAAACATCTGCGCTAATGTTCCAGATCCTTCAAGA 2224
 1858 GTAGTATAGCCACATGG 1874
 2225 GTCAATTTGCCACGTGG 2241

RESULT 3

US-09-058-263-1
 Sequence 1, Application US/09058263
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/058, 263
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/308, 881
 FILING DATE: 12-SEP-1994
 APPLICATION NUMBER: US 08/249, 553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2369 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B10G/PDC303
 FEATURE:
 NAME/KEY: CDS

LOCATION: 244..2369
 FEATURE:
 NAME/KEY: mat..peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig..peptide
 LOCATION: 244..309
 us-09-058-263-1

Query Match 4.0% Score 96.6; DB 2; Length 2369;
 Best Local Similarity 44.6%; Pred. No. 7.4e20;

Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

DB 724 CGTACACCTCAGCGGCTGCGAGCTTTTACAGAAATATGCTATGCTGCGATGCGG 783
 1091 CATTGCTGCTCAAGAGCTTTAACTTTTACAGAAATATGCTTGAAGTTGCTGTATGA 1150
 DB 784 TCAGAGAGTCAAG---TTCTGAGTGTAGTGGAGCCAGAAAGAAATGGAAATGACTGAG 840
 1151 AGGAAGATGTAGAGGATCTGAGTGTAGTGGAGGAGCAAGTGGATCAGCTATG 1210
 DB 841 AAGAAGTCCATGT---GGCTGGAAGTGTGAGAGTCTGAACCAAGCTGAGGGGATG 897
 1211 AAGATAGACCATTAACACCAAGTTCTGTATAAATAGATCCATCCATCTCAG 1270
 DB 898 GAAGAAGCCAGAGTGGGCTTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
 1271 GCTACAGAACTGTACAACTGCTGTGAGAGACATGCGCTCTTGAAGCCATGAGAAA 1330
 DB 958 CACTTGGCTACACATATGATGATCTATCCAGAAAGCAACATTAACCTCAGAGAAATGA 1017
 1331 TCTTGGATTAAGAGTGTACTCTCACAGATGAAATCAGATTACAAATTAACAGTTA 1390
 DB 1018 ACACACTAACACAGAGCTTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
 1391 ATGCCACAAAGTGA-----CAGTAATCTCACAAATGATCGCTATATACCAACCTTA 1444
 DB 1078 TTTCTTAATATCTCTTGGAGAGTCTCAGTGGCCAGCCCTGAGATTCAGATTCAAG 1137
 1445 CAGTAAGAAATCTTGTGGCAATCAGATGACAGTGTTTAAGTATCCCTGCTGAGT 1504
 DB 1138 AAAAATCTTTGAGTGTATGAGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1197
 1505 TTCAAGTACTACCTCTGTATGATCTTAAGCATCTCCCAAGATTAACGTTGGG 1564
 DB 1198 TGAAGTGCAAGAGCTGTCTAGACGTGAGACACTTGGATGATGAAGTTCGGATG 1257
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 DB 1258 TGGACCTGAGAGCCAGCAGCCCTTCTGGAATCTGTGTCTCAGGCCAGAGAGAGAG 1317
 1625 CAGATTAAGCAGCCCTGTATCAGAGCTGCAAGCAAGAGATGATGAGTGTGAGTGT 1684
 DB 1318 TCACAGCAAGATTAATTAACCTTCTGTGTCTATACATCTGTGTATCCAAATGTC 1377
 1685 ATTTAAGGAGGAACTTATACAGAGCAAGAAATCTATTTGATTAACGTTACTCAGTATATG 1744
 DB 1378 ATGACAAAGTTGGGAGGAGCATATTCATCCAGGCTTATGCCAAGAGGGCTTCATAG 1437
 1745 CTGATGAGACAGAGAGCCCTTAATTCATTAAGGCAATACCTTAACAGAGCTCCACCTTCA 1804
 DB 1438 AAGGTCTGAGACCAAGGTGAGAAATTTGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1497
 1805 AAGGACCTACTGTTGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1864
 DB 1498 AGATTCCAG 1557
 1865 AACTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1924
 DB 1558 AAGGAG 1617
 1925 TCATTGGAATGAAGT 1984

DB 1618 CCTGAAG 1677
 DB 1985 CTTTGAGTACAG 2044
 DB 1678 CCAAGGAG 1737
 2045 AGGATGCTCAGAAATTAACCTTTTACTACCCAAAGTTGCTCAAGAGAGAGAGAGAG 2104
 DB 1738 TAACCTCTGATGAG 1797
 2105 TAGTGTGCTGCTGTTGCTTACATCTTATGACAGAGAGAGAGAGAGAGAGAGAGAG 2164
 DB 1798 TCAAAAG 1857
 2165 TTAATTAAG 2224
 DB 1858 GTAGTATAGCCAGATG 1874
 2225 GTCATATGCCCCAGTGG 2241

RESULT 4

us-09-059-099-1

; Sequence 1, Application US/09059099

; Patent No. 5925740

; GENERAL INFORMATION:

; APPLICANT: Mosley, Bruce

; APPLICANT: Cosman, David J.

; TITLE OF INVENTION: Receptor for Oncostatin M

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,099

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

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TOPOLOGY: linear

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HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TISSUE TYPE: human placenta

IMMEDIATE SOURCE:

CLONE: B10G/PC303

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? : FEATURE:
? : NAME/KEY: CDS
? : LOCATION: 244..2369
? : FEATURE:
? : NAME/KEY: mat_peptide
? : LOCATION: 310..2369
? : FEATURE:
? : NAME/KEY: sig_peptide
? : LOCATION: 244..309
US-09-059-099-1

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Query Match	4.0%;	Score 96.6;	DB 2;	Length 2369;
Best Local Similarity	44.6%;	Pred. No. 7.4e-20;		
Matches 516;	Conservative 0;	Mismatches 629;	Indels 12;	Gaps 3;

QY	724	CGTCAACCTTCACGGGGGTGCAGCCTTTTACAGAAATATGTCATACCTCTGGCATGTGGGG	783
Db	1091	CATTCACTGTCCAGACCTTAACCTTTTACAGAAATATGTGTTTAAAGATTGCGTCTATAGA	1150
QY	784	TCAAGAGTCAAG---TTCTGAGTGCAGTGGAGCCAGAAAAATGGGAATGACTGAG	840
Db	1151	AGGAAGCTGCATGT---GGCCTGGACCTGTGGAGAGTCTGAATCCACTGAGGGGATG	897
QY	841	AAGAAGCTGCATGT---GGCCTGGACCTGTGGAGAGTCTGAATCCACTGAGGGGATG	897
Db	1211	AAGATTAGACACTTAAAGCCACCAAGTTTCTGGTATAAATATGATCCATCCATCTCAAG	1270
QY	898	GAAGAAGGCCAGTGCAGTTTGTATGAGAAAGCAAGAAGAGGCCACGCTCCAGAGAAA	957
Db	1271	GCTACAGAACTGTACAACTCGTGTGGAAAGACATTTGCCCTTTTGAACCAATGGAAAA	1330
QY	958	CACCTGGCTACACATATGTGACTATCCAGAAAGCACATPACTCAGAGAAACATGA	1017
Db	1331	TCCTTGATTTATGAAAGTGCATCTCAAGAGATGGAAATCACATTTTCAAAATTTACACAGTTA	1390
QY	1018	ACACTTACATCAACAGAGCTTGAACCTGCATCGTGGAGGGAGAGCTTTTGGGTGTATGA	1077
Db	1391	ATGCCACAAAACCTGA-----CAGTAAATCTCACAAATGATGCGCTATGTACGAACCCCTPA	1444
QY	1078	TTTCTTATATTTCTTGGGAAGTCTCCAGTGGCCACCCCTGAGATTCACAGTATTCAG	1137
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QY	1138	AAAAATCATTTTCAGTGCATTGAGTTCATGACAGCCCTGCGTTGCTGGAGACCAAGTATGG	1197
Db	1505	TTTCAAGTACTACCCCTGTATGATGATTTAAAGCATTTCCCAAGATPAACATGCTTTGGG	1564
QY	1198	TGAAGTGGCAAAAGCTCTGCTCTAAGACGTGAACACTTGGATGTATATATGTTCCGATG	1257
Db	1565	TGGATGGACTATCTCCAAAGGAATCTGTAAGAAATATATATCTTGAGTGGTGTGTTAT	1624
QY	1258	TGAGCTCAGAGCCACCAACCCCTTTCCTGGGAATCTGTCTCAGAGCCACGAATCGACGA	1317
Db	1625	CAGATTAAGCAACCCCTGTATCAGACAGTGGCAACAAGATGTGTACCTGCTGATGCACTT	1684
QY	1318	TCACGCAAGATTAATTAAACCTTTCTGTGCTATATACATCTCTGTATCCAAATGTTGC	1377
Db	1685	ATTTAAGGGGAACTGTAGCAGAGACCAATCTATTGTATTAACATTTACTCCAGATATWG	1744
QY	1378	ATGACAAAGTTGGGGAGCCATATTCATCCACGGTTATGCCAANAAGCCGTTCCATCAG	1437
Db	1745	CTGATGGACAGGAAGCCCTGAATCCATPAAGGCATTACCTTAAACAACTCCACCTTCCA	1804
QY	1438	AAGTCTCTGAACCAAGGTGGAGAAACATTTGGCGTGAAGAGCGTCCAGATCACTAGAGAA	1497
Db	1805	AAGGACCTACTCTTGGACCAAAAAAAGTAGGAAAAACGAAGCTGTCTTAGAGTGGAGC	1864
QY	1498	AGATTCCCAAGAGTAGAGAAAAGGGTATCATCTGCACATPACACATCTTTTACCAAGCTG	1557
Db	1865	AACCTCTGTTGATGTTCCAGATGAGATTATTCAGAAATTTATACATTTTATAGAACCA	1924
QY	1558	AAGGTGAAAAAGATTTCTCAAGACAGTCATTTCCAGATCTTGGAGTAGAGGCTGAGCT	1617

Db	1925	TCATTGGAAATGAAGAACTGCCTGTAATGGATTCCTTCCACACAGAAATATTCATTTGTCCT	1984
Qy	1618	CCCTGAAACCAAGAAACCTCTTACATTTGTTCAAGCATATGGCCAGACACCAGTCTCTGGGGAA	1677
Db	1985	CTTTGACTAGTGAACACATGTACATGTGACGAATGGACGATTCACAGATGAATGAAGCTGGGA	2044
Qy	1678	CCAACGGGACCAGCATAAATTTCAAGACATTTGATTCAGTGTCTTTGAGATTTATCCGCA	1737
Db	2045	AGGATGTGTCAGAAATTCACCTTTTCTTACTACCCCAAGTTTGGTTCAGAGGAAATTTGAAGCA	2104
Qy	1738	TAACTTCTCTGATGTGGTGGAGCCCTCTTATTCATTCATTCCTGACAGTGGCATATGTC	1797
Db	2105	TATGTCGTGCCCTGTTTGCTTTAGCATTTCCATTGACACACTCTTGTGGAGTGTGTTGCT	2164
Qy	1798	TCAAAAAAACCCACMAAAATTGACATCATCTGTGTGGCCACCGTTCGCCAACCCCTGCTAAA	1857
Db	2165	TTAATTAAGCGAGACCTTAATTAATAAACACATCTGGCTAAATGTTCACGATCCTTCAAGA	2224
Qy	1858	GTAGTATAGCCACATGG	1874
Db	2225	GTCAATATTTGCCCACTGG	2241

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1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

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IMMEDIATE SOURCE:
CLONE: B10G/PC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-058-264-1

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Query Match      4.0%; Score 96.6; DB 3; Length 2369;
Best Local Similarity 44.6%; Pred. No. 7.4e-20;
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

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QY 724 CGTCAACCTGACGGGCTGACGCTTTTACAGAAATATGCTATGCTGCGATGCGG 783
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DB 1091 CATTCACTGTCACAGACCTTAAACCTTTTACAGAAATATGCTATGCTGCTATGA 1150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 784 TCAGAGTCAAG---TTCTGAGTACTGAGCCCAAGAAATAATGGATGACTGAG 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1151 AGGAAGATGGTAAGGATACCTGAGTACTGAGTGAAGAGCAAGTGGATCACTATG 1210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 AAGAAGCTCATGT---GGCTGGAAGTGGAGATGCTGAACCAAGCTGAGCGGATG 897
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1211 AAGTATAGACCATTAAGACCAACCAAGTTCTGATTAATAATGATCCATCCATCAAG 1270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 898 GAGAGAGCCAGTCGGCTGTTATGAGAGAGCAAGAGAGAGCCAGTCTAGAGAAA 957
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1271 GCTACAGACGTGTCAACTGCTGTGGAAGACATTCCTCTTTTGAAGCCAAATGAAAA 1330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 958 CACTTGGCTACACATATGTGACTATCCAGAAACACACATACCTCAGAAACATGA 1017
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1331 TCTTGGATTATGAGTACTCTCACAAGATGGAATACATTTACAAATTTACACATTA 1390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1018 ACACCTACTAACAGACAGCTTGAACTGATCTGGAGGAGAGAGCTTTGGGTCTATGA 1077
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1391 ATGCCACAAAACCTGA-----CAGTAATCTCACAATAATGATCGTATCTGACACCTTA 1444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1078 TTTCTTTAATTCCTCTGGGAAGTCTCAGTGGCCACCTGAGGATTCACATTTCAAG 1137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1445 CAGTAAAGAAATCTTTGGGCAAAATCAGATCAGCTGTTTAACTATCCCTGCTGACT 1504
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QY 1138 AAAATATCTTCAGTGCATTGAGGTCAATGACAGCCCTGCTGAGAGACAGCTAGTG 1197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1505 TTCAAGCTACTACCTCTGTAATGATCTTTAAGCATTCCTCCAAAGATTAACGTCTTGGG 1564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1198 TGAAGTGGCAAGCTCTGCTCTAGACGTGAACACTTGATGATTAATGTTTCCGGATG 1257
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DB 1565 TGAATGAGTACTACCAAGGAATCTGTAAAGAAATATTAATCTGAGTGGTGTGTAT 1624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1258 TGGACTAGAGCCACCACTTCTCTGGGAATCTGTGCTCAGGCCACGAATGAGCA 1317
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DB 1625 CAGATTAAGAACCTGTATCACAACACTGGCAACGAAGAATGTGATCGATCGCACT 1684
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QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGCTATTAACATCTGCTGATATCCATGTGC 1377
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DB 1685 ATTTAAGAGGAACTTATGACAGAGCAATATGCTATTTGATTAACAGTACTCCATATATG 1744
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QY 1378 ATGACAAAGTTGGGAGCATATTCATCCAGGCTTATGCAAGAGAGGCTTCCATCAG 1437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1745 CTGATGACAGGAGAGCCCTGAATTCATTAAGGATACCTTAACAAGATTCACCTTCCA 1804
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QY 1438 AAGTCTCTGAGACCAAGGTGAGAACATTTGGCGTGAAGAGGCTCAGCATACATGAAG 1497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1805 AAGGACCTACTGTTCGACAAAAAAGTAGGAAAAAGCAAGCTGTCTTAGAGTGGAGC 1864
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1498 AGATTCACAGAGTGAAGAGAGGTATCATCTGACACTACACATTTTACCAAGCTG 1557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1865 AACTTCTGTGTGATGTTCAAGAAATGATTTATCAGAAATTAATTAATTAAGAACCA 1924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 1558 AAGTGGAAAAAGATTCCTCAGACAGTCAATTCACAGATCTTCAGTACGGCTGGAGT 1617
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DB 1925 TCATTGGAATGAAGACCTGCTGATATGGAATTTCTTCCACACAGAAATATCATTTGCT 1984
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QY 1618 CCTTGAAGCAAGACCTTTACATTTGTCAGGTATGCGCCAGCAGCAGCTGCTGGGAA 1677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1985 CTTTGACTAGTACACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2044
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1678 CCAAGGAGCAGATTAATTTCAAGACATTTGATTCAGTGTCTTTGAGATTTCTCA 1737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2045 AGGATGTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1738 TAACCTCTGATTTGATGAGAGGCTTCTTATTCATTAATTCATTAATTCATTAATTC 1797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2105 TAGTGTGAGCTGTTTGTCTTACATTCATTAATTAATTAATTAATTAATTAATTAATTA 2164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1798 TCAAAAAACCAACAAATTCATCTGTTGTTGGCCACCGTTCCCAACCTGCTGAAA 1857
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2165 TTAATTAAGCAGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1858 GTAGTATAGCCACATGG 1874
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2225 GTCAATTTGCCAGTGG 2241
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RESULT 6
US-09-455-962-1
Sequence 1, Application US/09455962
Patent No. 6524817
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,962
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,264
FILING DATE:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

```

```

ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 244..309
US-09-455-962-1

Query Match 4.0%; Score 96.6; DB 4; Length 2369;
Best Local Similarity 44.6%; Pred. No. 7.4e-20;
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTACAACTTCACGGGCTGACGCTTTTACAGATATGTCATAGCTCTGCGATGCGG 783
DB 1091 CATTCACGTGTCAGACCTTTTACAGATATGTCATAGCTCTGCGATGCGG 1150
QY 784 TCAAGAGTCAAG---TTCTGGAGTACTGAGCCAGAAAATGGGAATGACTGAG 840
DB 1151 AGGAAGATGATGAAGGATGAGTACTGAGTACTGAGGAAGCAAGTGGGATCACTATG 1210
QY 841 AAGAAGTCCATGT---GGCCTGGAAGTCTGAGAGTCTGGAACCAAGCTAGGCGATG 897
DB 1211 AAGTATAGACATCTTAAGACACCAAGTTTGTGTATTAATAATGATCCATCCATCTCAAG 1270
QY 898 GAAGAAGGCCAGTGCAGTTGTTATGAAAGCAAGAGAGAGCCAGTCTTAGAGAAA 957
DB 1271 GCTACAGAGCTGTACACTGCTGTGGAAGACATTGCCCTTTGAGGCCAATGAAAA 1330
QY 958 CACTTGGCTACACATATGCTACTATTCAGAAAGCAACACTAACCTACAGAAAATGA 1017
DB 1331 TCTTGGATTTATGAAGTACTCTCACAAGATGAATACATTTCAAAATTAACACAGTTA 1390
QY 1018 AACTACTAACCCAGCAGCTTGAAGTATGAGGAGGAGAGAGTTTGGGTGCTATGA 1077
DB 1391 ATGCCACAAAAGTCA-----CAGTAATCTCACAAATGATGCTATCTACAAACCTTA 1444
QY 1078 TTTCTTAATTTCTTGGGAAGTCTCCAGTGCACCCCTGAGGATTCACACTATTCAG 1137
DB 1445 CAGTAAGAATCTTGTGGCAAAATCAGATGAGCTGTTTAACTATCCCTGCTGACT 1504
QY 1138 AAAAATCATTTCACTGATGAGTCAATGACAGGCTGCTGAGAGCAGCTAGTGG 1197
DB 1505 TTCAAGTACTCACCCCTGTATGATCTTAAAGCATTCGCCCAAGATTAACATGCTTGGG 1564
QY 1198 TGAAGTGCAAAAGCTGTCTAGACGTGAACACTTGGATGATGAATGGTTCCGGATG 1257
DB 1565 TGGATGAGTACTCTCCCAAGGAATCTGTAAAGAAATATATCTTGAAGTGGTGTAT 1624
QY 1258 TGAAGTGAAGCCAGCACCCTTCTGGAATCTGTGTCTCAGGCCAGAACTGAGCA 1317
DB 1625 CAGATTAAGACACCTGTATCAGACTGAGCAAAAGAAAGATGACGCTGATGGCACT 1664
QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGCTTAAACATCTGTGTATCCAAATGTTGC 1377
DB 1685 ATTTAAGAGGGAACCTTGAAGAGAGCAAAATGCTATTGTATTAACAGTACTCAGATATG 1744
QY 1378 ATGACAAAGTTGGGAGCATATTCATCCAGGCTTTTGGCAAAAGAGGCTTCCATCAG 1437
DB 1745 CTGATGAGACAGGAAGCCCTTAATCCATTAAGGCAATACCTTAACAGAGCTCCACCTCA 1804
QY 1438 AAGGTCTGAGACCAAGCTGAGAAACATTTGGCGTGAAGACGCTCAGATCAGTGAAG 1497
DB 1805 AAGGACCTACTGTTGCGCAAAAAGAGTGAAGAAAAGAAAGAGTGTCTTAAGTGGAGCC 1864
QY 1498 AGATTCCCAAGAGTGAAGAAAGGTATCATCTCTCAGCACTACACATCTTTTACCAAGCTG 1557

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DB 1865 AACTTCCGTGATGTTCCAGATGATTTATCAGAAATTAATACTATATTTATAGAACCA 1924
QY 1558 AAGGTGAAAGATTTCTCCAGACAGTCAATTCAGATCTTCCAGTACGCCCTGAGT 1617
DB 1925 TCATTGGAAATGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1984
QY 1618 CCTGAAAGCAAGACCTCTTACATTTGCTCAGTCAATGAGCAGCAGCAGCAGCAGCAGCAG 1677
DB 1985 CTTGAGTACAGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2044
QY 1678 CCAAGGAGCAGCAGATTAATTTCAAGACATTTGATGATGATGATGATGATGATGATGAT 1737
DB 2045 AGGATGCTCCAGATTTACTTTTACTACCCCAAGTTGCTCAAGAGAAATGGAAGCA 2104
QY 1738 TAACCTCTGATGTTGGAGGCGCTTCTTATTCATTAATCCAGAGTGCATATGTC 1797
DB 2105 TAGTCGTCCTGTTGCTTACATTTCCATTTGACAACTCTTGTGGAGTGTGTTGCT 2164
QY 1798 TCAAAAAACCCAAACAAATGACATCTGTTGGCCACCCAGTCCCAACCTGCTGANA 1857
DB 2165 TTATTAAGCAGACCTATTTAAACACATCTGCGCTAATGTTCCAGATCTTCAANA 2224
QY 1858 GTACTATAGCCCATG 1874
DB 2225 GTCAATATGCCCAGTGG 2241

RESULT 7
PCT-US95-06530-1
Sequence 1, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

```

FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B106/pDC303
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 244..2369
 FEATURE:
 NAME/KEY: mat.peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig.peptide
 LOCATION: 244..309
 PCT-US95-06530-1

Query Match 4.0%; Score 96.6; DB 5; Length 2369;
 Best Local Similarity 44.6%; Pred. No. 7.4e-20;
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 GTCACACCTCAGCGGCTGAGCCTTTACAGATATGTCATACCTCTGGATGCGG 783
 DB 1091 CATTCACGTCCAGACCTTTAACTTTACAGATATGTTTGAATGCGCTGATGA 1150
 QY 784 TCAAGAGTCAAG--TTCTGAGTACTGAGCCAGAAAAATGGAAATGACTGAG 840
 DB 1151 AGAAGATGTAGAGGATAGTGAAGTGAAGCAAGTGGATCACCATTG 1210
 QY 841 AAGAAGCTCCATGT---GGCCTGAGACTGTGAGAGTCTGTAACCACTGAGCGGATG 897
 DB 1211 AAGATAGACCAATTAACACCAGATTCTGTATTAATTAATGATCCATCCATCTCAAG 1270
 QY 898 GAAGAGGCCAGTGGGTTGTTATGAGAAAGCAAGAGAGCCAGTCCAGAGAAA 957
 DB 1271 GCTACAGAACGTACAACTCGTGTGAGACATTGCCCTTTGAGCCATGAAAAA 1330
 QY 958 CACTTGGCTACACATATGTACTATCCAGAAAGCAACATGACTACAGAAACATGA 1017
 DB 1331 TCTTGATATGAAAGTACTCTCACAAAGATGAAATCAATTTACAAATTTACACAGTTA 1390
 QY 1018 ACACACTAACACAGAGCTTGAACGTCTGGAGGAGAGAGCTTTGGGTGCTGTATGA 1077
 DB 1391 ATGCCCAAAACTGA-----CAGTAAATCTCACAAATGATGCGTATCTACAAACCTTA 1444
 QY 1078 TTTCTTAATATCTCTTGGGAATCTCCAGTGGCCACCTGAGATTTCCAGTATTTCAAG 1137
 DB 1445 CAGTAAAGAAATCTTGTGGCAATTCAGATGACAGTGTTTAACTATCCCTGCTGTGACT 1504
 QY 1138 AAAAATCTTTCAGTGTGATGATGATGAGCCCTGCTGTTGAGAGACCACTAGTGG 1197
 DB 1505 TTCAAGCTACACCTCTGTATGATCTTAAGCATTCCTCCAAAGATTAACATGCTTTGGG 1564
 QY 1198 TGAAGTGGCAAGGCTCTGCTAGACGTGAACACTTGGATGATGAATGATTTCCGGATG 1257
 DB 1565 TGGATGAGTACTACTCCAAAGGAATCTGTAAGAAATATATCTTGAGTGGTGTGTTAT 1624
 QY 1258 TGAAGTCAAGCCCAACACCTTTCTGGGAATCTGTCTTCAGGCCACGAACTGAGAGA 1317
 DB 1625 CAGATTAAGGACACCTGTATTCACAGCTGGCAACAAGATGATGACCTGATGACACT 1684
 QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGCTTATACATCTCTGTATGATCAATGTTGC 1377
 DB 1685 ATTTAAGGGAATCTTACAGAGAGCAATATCTTATTAACAGTTACTCCAGATATG 1744
 QY 1378 ATGACAAAGTTGGGAGGCATATTCACAGGCTTATGCCAAGAAAGGCTTCCATGAG 1437
 DB 1745 CTGATGGACCAAGAGCCCTGAATCCATAAAGGATACCTTAACAAACCTCCACCTTCCA 1804
 QY 1438 AAGTCTCGAGACCAAGGTGAGCAACATTTGCGTGAAGACGTCACATCATGAGAAAG 1497
 DB 1805 AAGGACCTACTGTTGCGACAAAGAAAGATGAGAAAGAAAGAGCTGCTTTAAGTGGGACC 1864
 QY 1498 AGATTCCCAAGATGAGAGAAAGGATATCATCTGCACATCACTTTTACCAAGCTG 1557

DB 1865 AACTTCTGTGATGTTCAGATGATTTATCAGAAATTAATATATTTATATACACCA 1924
 QY 1558 AAGGTGAAAAAGATTTCTTCCAGACAGTCAATTCAGACATCTTGACATGACCCCTGGAGT 1617
 DB 1925 TCATTGAAATGAAGAACTCTGTGAATGTGATTTCTCCACACAAATATTCATGTCTC 1984
 QY 1618 CCTGAAGCAAGACCTCTTACATTTGTCAGGTGATGCCACGACAGTGTGGGGGA 1677
 DB 1985 CTTTGACTAGTACACATTTGTACATGTGATGATGCGACATACACATAGAGTGGGA 2044
 QY 1678 CCAAGGAGCAGCAGATAAATTTCAAGACATTTGCAATTCAGTGTCTTTGAGATTATCTCA 1737
 DB 2045 AGGATGCTCCAGAAATTAATCTTTTACTACCCCAAGTTTGTCAAGAGAAATGAAGCCA 2104
 QY 1738 TAACCTCTGATTTGTGAGAGCCCTTCTTATTTCTATTCATTCCTGACAGTGCATATGCTC 1797
 DB 2105 TAGTCGTGCTGTTGCTTACATTCCTATTGACAACTCTTGTGAGATGCTGTCTGCT 2164
 QY 1798 TCAAAAAACCCCAAAATTTGATCTATCTGTGTCGCGCCACCGTTCCCAACCTGCGTGA 1857
 DB 2165 TTAATACGCGAGACCTAATTTAAAAACATCTGCGCTTAATGTTCCAGATCTTTCAAGA 2224
 QY 1858 GTAGTATGCCACATG 1874
 DB 2225 GTCATATTGCCAGTGG 2241

RESULT 8

US-08-825-558-5
 ; Sequence 5, Application US/08825558
 ; Patent No. 5965724

GENERAL INFORMATION:

APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/825.558
 FILING DATE: 19-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: ESMOND, ROBERT W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0623.0530001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2754 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2754

US-08-825-558-5

Query Match 4.0%: Score 96.6; DB 2; Length 2754;
 Best Local Similarity 44.6%; Pred. No. 8.1e-20;
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTCAACCTCAGGGGCTGCAGCCTTTTACAGAAATGTCATAGCTCTGCGATGCGG 783
 DB 848 CATTCACTGTCGAAGACCTTAACCTTTTACGAATATGTTGTAGATTCGCTATGA 907
 QY 784 TCAAGAGTCAAG---TTCTGAGTGTGAGTGCAGCAAGAAATGGAATGACTGAG 840
 DB 908 AGGAAGATGTGAAGGATACGTGAGTACTGAGATGAGAGCAAGTGGATCCATG 967
 QY 841 AAGAAGTCCATGT---GGCCTGGAAGTGTGAGAGTCTTGAAACCAAGCTGAGCGGATG 897
 DB 968 AAGATAGACCATTAAGACCAAGTTTCTGTATTAATAATGATCCATCCATCTCAAG 1027
 QY 898 GAAGAAGCCAGTCCGCTGTTTATGAGAAAGCAAGAGAGCCCACTCTAAGAAAA 957
 DB 1028 GCTACAGACCTGTCAACACTGCTGTGGAAGACATTCCTCTTTTGAAGCCAAATGAAAA 1087
 QY 958 CACTTGGCTCAACATATGTAATTCGAGAAAGCAACACTAACCTCACAAGCAATGA 1017
 DB 1088 TCTTGATATTAAGAGTACTCTCAAGATGGAATACATTTTCAAAATTTACACAGTTA 1147
 QY 1018 ACACCTACTAACCAAGCTTGAACTGCATCTGGAGAGCGAGCTTTTGGTGTCTATGA 1077
 DB 1148 ATGCCACAAAACCTGA-----CAGTAATCTCACAAATGATCGTATCTACCAACCTTA 1201
 QY 1078 TTTTCTTAATTTCTTGTGGAGAGTCTCAGTGGCCACCCTGAGATTCACATATCAAG 1137
 DB 1202 CAGTAAGAAATCTTGTGGCAAAATCAATGACGCTGTTTAACTATCCCTGCTGACT 1261
 QY 1138 AAAATCATTTTCAGTGAATGAGTGCATGCGAGCCTGGCTGGAGAGCAGCAATGAG 1197
 DB 1262 TTCAAGCTACTACCCCTGTATGATCTTTAAAGCATTCGCCAAAGATTAACATGCTTGG 1321
 QY 1198 TGAAGTGGCAAGCTGTGCTCTAGACGTGAACACTTGGATGATGAATGGTTCCGATG 1257
 DB 1322 TGAATGAGACTACTCCAAAGGAACTGTGAAGAAATATATCTGAGTGGTGTAT 1381
 QY 1258 TGGACTGAGAGCCCAACCTTTCTGGGAATCTGTCTCAGGCCACGAACTGAGCA 1317
 DB 1382 CAGATTAAGCACCTGTATCAGACGTGGCAACAAAGATGATCCCTGATGCACT 1441
 QY 1318 TCCAGCAAGATTAATTAACCTTTCTGCTGTATACATCTGTGTATCCAAATGTC 1377
 DB 1442 ATTTAAGAGGAACTTACAGAGCAAGCAATGCTATTTGATACAGTTACTCCAGTATG 1501
 QY 1378 ATGACAAAGTTGGAGGACCATTTCCATCCAGCTTATGCCAAGAAAGGCGTTCATCAG 1437
 DB 1502 CTGATGAGCCAGAAAGCCCTGAATCCATTAAGGCATACCTTAACACAGCTCCACCTTCA 1561
 QY 1438 AAGTCTCTGAGACCAAGGTGGAACATTTGGCTGGAAGAGCGTCAACATCAGTCAATG 1497
 DB 1562 AAGGACCTACTGTCGGCAAAAAGAGGAAAAAGAGAGCTGTCTTAAGTGGGACC 1621
 QY 1498 AGATTCGCAAGAGTGAAGAAAGGTATCTGCACTACACTACACATCTTTACCAAGCTG 1557
 DB 1622 AACTTCTGTTGATGTTTACAGATGATTTATCAGAAATTAATATATATTTATGAACCA 1681
 QY 1558 AAGGTGGAAGAGATTTCCAGAGACATTCAGATTCAGATTCAGTACGCGCTGAGT 1617
 DB 1682 TCATTTGGAATGAAGATGCTGTGATGATGATTTCTTCCACACAGAAATATACATTTGCT 1741
 QY 1618 CCCGGAAGCAAGAACTCTTACATTTGTCAGTCAATGCGCAGCAACAGTCTGAGGGGAA 1677
 DB 1742 CTTTGACTAGTGAACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1801
 QY 1678 CCAAGGAGCAGCAGATTAATTTCAAGACATTTGATGATGATGATGATGATGATGATG 1737
 DB 1802 AGGATGTCAGAAATTCATTTTACATCCCAAAAGTTTCTCAAGAGCAAAATTTGAACCA 1861
 QY 1738 TAACTTCTCTGATTTGTGAGGCGCTTCTTATTTCTCATTTATCCCTGACATATGCTC 1797

DB 1862 TAGTCGTGCTGTTGCTTACATTTCCATTTGACACACTCTTCTGGAGTGTGCTGCT 1921
 QY 1798 TCAAAAAACCAACAAATTTGATCTGTGTGTTGGCCACCGCTTCCCAACCTCTGAAA 1857
 DB 1922 TTAATTAAGCGAGACCTTAATTAATAACATCTGCTTAATGTTCCAGATCTTTCAAGA 1981
 QY 1858 GTACTATAGCCACATGG 1874
 DB 1982 GTCATATTTGCCAGTGG 1998

RESULT 9
 US-09-312-611-5
 Sequence 5, Application US/09312611
 Patent No. 6380160
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/312.611
 FILING DATE: 17-MAY-1999
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: ESKOND, ROBERT W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0623.0530002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 TELEFAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2754 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..2754
 US-09-312-611-5

Query Match 4.0%: Score 96.6; DB 4; Length 2754;
 Best Local Similarity 44.6%; Pred. No. 8.1e-20;
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTCAACCTCAGGGGCTGCAGCCTTTTACAGAAATGTCATAGCTCTGCGATGCGG 783
 DB 848 CATTCACTGTCGAAGACCTTAACCTTTTACGAATATGTTGTAGATTCGCTATGA 907
 QY 784 TCAAGAGTCAAG---TTCTGAGTGTGAGTGCAGCAAGAAATGGAATGACTGAG 840
 DB 908 AGGAAGATGTGAAGGATACGTGAGTACTGAGATGAGAGCAAGTGGATCCATG 967
 QY 841 AAGAAGTCCATGT---GGCCTGGAAGTGTGAGAGTCTTGAAACCAAGCTGAGCGGATG 897
 DB 968 AAGATAGACCATTAAGACCAAGTTTCTGTATTAATAATGATCCATCCATCTCAAG 1027

QY 898 GAAGAGCCAGTGGCTGTTGATGGAAGAGGAGAGGAGCCCACTGCTAGAGAAA 957
DB 1028 GCTACAGAACTGTACAACTCGTGTGGAAGACATTGCCCTTTGGAACCAATGGAAGAAA 1087
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QY 1018 ACACCTAAACACAGAGCTTGAAGTGCATCTGGAGGAGAGGAGCTTTGGTGTCTATGA 1077
DB 1148 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATCGCTATCTACCAACCTTAA 1201
QY 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCACCTATTCAAG 1137
DB 1202 CAGTAAGAAATCTTGTGGCAAAATCAGATGCGAGTGTAACTATCCCTCGTGTACT 1261
QY 1138 AAAATATCTTCACTGATGATAGTGCATGAGGCTGCTGTGCTGAGGAGCAGCTAGTGG 1197
DB 1262 TTCAAGCTACTACCCCTGTATGATCTTAAGCATTCGCCCAAGATTAACATGCTTGGG 1321
QY 1198 TGAAGTGCAGAAAGCTGCTCTAGACGTGAACACTGTGATGATGAATGTTCCGGATG 1257
DB 1322 TGGATGAGCTACTCTCCAGAGGAATCTGAAGAAATATATCTTGAAGTGTGTCTTAT 1381
QY 1258 TGAAGTGCAGAGCCAGCACCCTTCTGGAATCTGTCTCAGGCGCAGAACTGAGAGA 1317
DB 1382 CAGATTAAGACACCTGTATCAGAGCTGGCAAGAAAGATGATGATGATGATGATGATG 1441
QY 1318 TCCAGCAAGATTAATTAACCTTCTGTGTCTATACATCTCTGTGTATCCATGTTGC 1377
DB 1442 ATTTAAGGGGAGACTTGTGACAGAGCAAAATCTTATGATTAACAGTTACTCCATTAATG 1501
QY 1378 ATGACAAAGTTGGCGAGCATATTCATCCAGCTTATGCCAAAGAGGCTTCCATCAG 1437
DB 1502 CTGATGAGACCGAGAGGCCCTTAATCCATTAAGCATACCTTAACAGACTCCACTTCA 1561
QY 1438 AAGTCTGAGACCAAGGTGAGAACATTTGGCTGAAGACGCTCAGATCATGGAAG 1497
DB 1562 AAGACCTACTGCTGCGCAAAAAGATGAGGAAAGAGAGAGCTGTCTTGAAGTGGACC 1621
QY 1498 AGATTTCCAGAGTGAAGAGAGGATTCATCTGCACATACCATCTTTTACCAAGCTG 1557
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QY 1558 AAGTGTGAAGAGATTTCTCAAGACAGTCAATTCAGCATCTTCCAGTACGCGCTGAGT 1617
DB 1682 TCATTTGGAATGAAGTGTGTGATGTGATGATCTTCCACACAGAAATATCATTTGCT 1741
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DB 1742 CTTTGAAGTGAAGACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1801
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DB 1802 AGGATGCTCCAGAAATTAATTTCACTTACTACCCCAAGGTTTGTCTCAAGAGAAATTAAGCA 1861
QY 1738 TAACCTCTGATTTGTGAGAGGCTTCTTATTTCAATATCTGACAGATGATGATGATG 1797
DB 1862 TAGTGTGCTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1921
QY 1798 TCAAAAAACCAACAAATTTGATCTGTGTTGGCCACCGTTCCCAACCTGCTGAAA 1857
DB 1922 TTAATTAAGCGAGACCTTAATTAAGAAACATCTGGCTTAATGTTCCAGATCTTCAAGA 1981
QY 1858 GTAGTATAGCCACATGG 1874
DB 1982 GTCAATTTGCGCACTGG 1998

RESULT 10
US-08-795-4738-4
Sequence 4, Application US/087954738
Patent No. 6217858

GENERAL INFORMATION:
APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,4738
FILING DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963,1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-795-4738-4
Query Match 4.0%; Score 96.6; DB 3; Length 3085;
Best Local Similarity 44.6%; Pred. No. 8.7e-20;
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;
QY 724 GGTACAACTGACGAGGCTGACGCTTTTACAGATATGTCATGCTGTGATGTCGG 783
DB 1103 CATTCACGTGTCAGACCTTAACCTTTTACAGATATGTTTGAAGTTGCTGTATGA 1162
QY 784 TCAAGGATCAAG---TTCTGAGTGTGATGAGCAGCAAGAAATGGAATGCTGAG 840
DB 1163 AGGAAGATGTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATG 1222
QY 841 AAGAAGCTCCATGT---GGCTGGAAGTGTGAGAGTCTTGAACCAAGCTGAGCGGATG 897
DB 1223 AAGATAGACCTCTTAAGGACCAAGTTTGTGATTAATATGATTCATCTCATCTCAAG 1282
QY 898 GAAGAGCCAGTGGCTGTTGATGGAAGAGGAGAGGAGCCAGCTCTAGAGAAA 957
DB 1283 GCTACAGAACTGTCAACTCGTGTGAAAGACATTTGCTTGTGAAGCCAAATGAGAAA 1342
QY 958 CACTTGGCTACACATATGTACTATTCAGAAAGCAGACATTAACCTCAGCAAAACATGA 1017
DB 1343 TCTTGATTAAGAGTGCATCTCACAGATGGAATGACATTTCAAAATTTACACAGTTA 1402
QY 1018 ACACCTAAACACAGAGCTTGAAGTGCATCTGGAGGAGAGGCTTTGGTGTCTATGA 1077
DB 1403 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATGCTATCTAGCAACCTTAA 1456
QY 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCAGATTTCAAG 1137
DB 1457 CAGTAAGAAATCTTGTGGCAAAATCAGATGAGCTGTTTAACTATCCCTGCTGACT 1516
QY 1138 AAAATATCTTCACTGATGATAGTGCATGAGGCTGCTGTGCTGAGAGCAGCAGTACTGG 1197
DB 1517 TTCAAGCTACTACCCCTGTATGATGATCTTAAGCATTCGCCCAAGATTAACATGCTTTGGG 1576

OY	1198	TCGAATGGCAAAAGCTGCTGCTCTACACGGAACTCTGGATCATGTAATGGTTTCCGAGT	1257
Db	1577	TGGATATGACTACTCTCCAAAGGAATCTGTAAAGAAATATATCTGAGTGGTGTATT	1636
OY	1258	TGGACTAGAGCCCGACACCCTTCTCGGAATCTGTGTCTCAGGCGACGAACTGGACGA	1317
Db	1637	CAGATTAAGACCCCTGTATCACAGACTGGCAACAAAGAAATGATGACGTGCATGGACCT	1696
OY	1318	TCCAGCAAGATTAATTAACCTTTCTGGTGCCTTAACATCTGTGTATTCAAATGTTGC	1377
Db	1697	ATTTAAGGGGAACTTTAGCAGAGAGCAAAATCCTATTGTATTAACGTTACTCCAGTATATG	1756
OY	1378	ATGCAAAAGTTGGCGAGCAGCATATTCATTCACAGGCTTATGGCAAGAAAGCGCTTCCATCG	1437
Db	1757	CTGATGGAGCCAGGAAGCCCTTAATTCATTAAGGCATACCTTTAAACAGCTCCACCTTCCA	1816
OY	1438	AAGTCTCTAGAACCAAGGTGGAGAACATTGGCGTGAAGACGGTCAAGTCATCATAAG	1497
Db	1817	AAGGACACTACTGTTCCGGACAAAAAAGATGGGAAAAAGAGCTGTCTTAAGTGGGACC	1876
OY	1498	AGATTCCCAAGATGAGAGAAAGGATATCATCTCACTACACCATCTTTTACCAAGGTG	1557
Db	1877	AACCTTCCTGTTGATGTTTCAGATGATTTATTCAGAAATTAATCTATATTTTATGAAACCA	1936
OY	1558	AAGGTGAAAAAGATTCTCCAAGACAGTCAATTCAGAGATCTCGACATGACGGCTGGAGT	1617
Db	1937	TCATTGGAAATGAACCTGCTGTGAATGGATGATCTTCCACACAGAAATATACATTTGCT	1996
OY	1618	CCCTGAAACGAAACACCTTACATTTGTTCAGGTACATGCGCAGACACCGCTCTGGGGAA	1677
Db	1997	CTTTGACTAGACACATTTGATACATGGTAGCAATGGCAGCATACAGATBAAGGTGGGA	2056
OY	1678	CCAACGGGACGACATAAATTTCAAGACATTTGATTCAGTCAAGTCTTTGAGATTATCTCA	1737
Db	2057	AGGATGGCCAGAAATTCACCTTTTACTACCCCAAGTTGTCACAGGAGAAATTTGAAGCA	2116
OY	1738	TAACTCTCTATATGCTGAGAGCCCTCTTATTTCTATATTCCTGACAGATGGCATATGGTC	1797
Db	2117	TATGCTGTCCTGTTTGGCTTTAGCATTTCTATTGACAACTCTTCTGGAACTGCTGTTCTCT	2176
OY	1798	TCAAAAAACCCACAAATTTGACATATCTGTGTGGCCACCGCTTCCCAACCTCTGAAA	1857
Db	2177	TTAATTAAGCGAGACCTAATTAAAAAACATCTGGCCCTTAATGTTCACAGATCCTTCAAGA	2238
OY	1858	GTAGTATAGCCACATGG	1874
Db	2237	GTCAATATGGCCAGTGG	2253

11 RESULT
 US-09-439-856-4
 : Sequence 4, Application US/09439856
 : Patent No. 6410009
 : GENERAL INFORMATION:
 : APPLICANT: Galun, Elhan
 : APPLICANT: Nahot, Orit
 : APPLICANT: Blum, Herbert E.
 : TITLE OF INVENTION: A Pharmaceutical Composition for Treating
 : TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Davidson and Kappel, LLC
 : STREET: 1140 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: MS-DOS EDITOR

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1  CURRENT APPLICATION DATA:
2  APPLICATION NUMBER: US/09/439,856
3  FILING DATE:
4  CLASSIFICATION:
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: 08/795,473
7  FILING DATE: 11-FEB-1997
8  ATTORNEY/AGENT INFORMATION:
9  NAME: Davidson, Clifford M
10 REGISTRATION NUMBER: 32,728
11 REFERENCE/DOCKET NUMBER: 963.1007
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (212)-997-1028
14 TELEFAX: (212)-997-1037
15 INFORMATION FOR SEQ ID NO: 4:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 3085 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: unknown
21 US-09-439-856-4
22
23 Query Match 4.0% Score 96.6; DB 4; Length 3085;
24 Best Local Similarity 44.6% Pred. No. 8,7e-20;
25 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;
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1438 AAGTCTGAGACCAAGGTGAGACATTTGGCGTGAGACGTCACGATCATCGAAG 1497
1817 AAGGACCTACTGTTGCGACAAAAAGTAGGAAAAAGAAAGCTCTTACAGTGGACC 1876
1498 AGATTCCCAAGAGTGAAGAAAGGTATCATCTGCACATCAACATCTTTTACCAAGCTG 1557
1877 AACTCCGTGATGATTCAGATGATTTATCAGAAATTAATCATATTTTATAGAACCA 1936
1558 AAGGTGAAAAGATTTCTCAAGACATTCACAGATCTTGAGTACGCGCTGGAGT 1617
1937 TCATTGGAATGAATCTGCTGTAATGATGATCTTCCACACAGAAATATCATTTGCT 1996
1618 CCGTAAAGCAAGACCTCTTACATTTGTCAGTCTGAGCCAGCACCAGCTCTGGGGAA 1677
1997 CTTGACATGAGACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 2056
1678 CCAACGGACACGATTAATTTCAAGACATTTGATGATGATGATGATGATGATGATG 1737
2057 AGGATGCTCAGAAATTCATCTTACTACCCCAAGTTGCTCAAGAGAAATTTGAAGCA 2116
1738 TAACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797
2117 TAGTCGCTGCTGTTGCTTACATTCATTTGATGATGATGATGATGATGATGATGATG 2176
1798 TCAAAAACCAACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1857
2177 TTAATGAACGAGACTTAATTAAGAAACATCTGCTGATGATGATGATGATGATGATG 2236
1858 CTAGATATGACCATG 1874
2237 GTCAATATGCGCCAGTGG 2253

RESULT 12

US-08-825-558-3
Sequence 3, Application US/08825558
Patent No. 5965724

GENERAL INFORMATION:

APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA

ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825.558

FILING DATE: 19-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0623.0530001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1977 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1974
US-08-825-558-3

Query Match 3.2%; Score 76.4; DB 2; Length 1977;
Best Local Similarity 44.5%; Pred. No. 1.6e-13;
Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

724 CGTACACCTACGGGCTGACACCTTTTACAGATATGATGATGATGATGATGATG 783
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968 AAGATGACACATCTAAGACACACAGTTTCTGATTAATAATGATGATGATGATGATG 1027
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QY 1678 CCAAGGGACGACATTAATTTCAGAC 1705
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Db 1802 AGGATGGTCCAGATTTCATTCTAC 1829

RESULT 13

US-09-312-611-3
: Sequence 3, Application US/09312611
: Patent No. 6380160
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: GP130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/312,611
: FILING DATE: 17-MAY-1999
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: ESMOND, ROBERT W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0623_0530002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2540
: TELEFAX: (202)371-2540
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1977 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1974
: US-09-312-611-3

Query Match 3.2% Score 76.4; DB 4; Length 1977;
Best Local Similarity 44.5% Pred. No. 1.6e-13;
Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

QY 724 CGTACAACCTCAGCGGCTCAGCCCTTTACAGAAATGTCATAGTCTGTGGATGTGCGG 783
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QY 898 GAAGAAGCCAGTCCGGTTGTTATGAAGAAGCAAGAGAGCCCAAGCTCTTAGAGAAA 957
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Db 1028 GCTACAGACTGTCACTGCTGTGGAAGACATTGCTCTTTGAAGCCATGAGAAAA 1087
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QY 1018 ACACCTACTAACGACAGCTTGAAGTGCATCTGGAGGCGAGAGCTTTGGGTGTATGA 1077
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Db 1202 CAGTAAGAAATCTTGTGGCAAAATCAGATCAGCTGTTTAACTATCCTCGCTGTGACT 1261
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QY 1138 AAAAATCATTTCAAGTGCATTAAGTCAATGACGCTGCTGTGAGGACCACTAGTGG 1197
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Db 1262 TTCAAGCTACTCAACCTGTAAATGATCTTAAGCATTCCTCCAAAGATTAACATGCTTTGGG 1321
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QY 1498 AGATTCCTCAAGAGTGAAGAGGATATCTGCAACTGCAACATCAACCATCTTTTACCAAGCTG 1557
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Db 1622 AACTTCTGTGATGTGACAAATGATTTATCAAGAAATTTATTAATTAATTAAGAACCA 1681
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QY 1558 AAGTGGAAAAAGATTTCCAGACATTCATTTCCAGATCTTGCATATGAGGCTGAGT 1617
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Db 1682 TCATTGGAATGAAGTCTGTGTAATGTGATTTCCACACAGAAATTAACATTTGCT 1741
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QY 1618 CCCTGAAGCAAGACCTCTTACATTTGTCAGTGCATGAGCAGCAGCAGCAGCTGGGAGAA 1677
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Db 1742 CTTGACTAGTGAACATTTGATGATGTTAGCAATGAGAGCATACAGATGAAAGTGGGA 1801
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QY 1678 CCAAGGGACCGACATTAATTTCAAGAC 1705
| | | | | | | | | | | | | | | | | |
Db 1802 AGGATGGTCCAGATTTCATTCTAC 1829
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RESULT 14

US-09-313-942-25
: Sequence 25, Application US/09313942
: Patent No. 6472179
: GENERAL INFORMATION:
: APPLICANT: REGENERON PHARMACEUTICALS, INC.
: TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
: FILE REFERENCE: REG 203-A
: CURRENT APPLICATION NUMBER: US/09/313,942
: PRIOR FILING DATE: 1999-05-19
: PRIOR APPLICATION NUMBER: 09/313,942
: PRIOR FILING DATE: 1999-05-19
: PRIOR APPLICATION NUMBER: 60/101,858
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 25
: LENGTH: 3477
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:

NAME/KEY: CDS
LOCATION: (1)...(3474)
US-09-313-942-25

Query Match 3.28; Score 76.4; DB 4; Length 3477;

Best Local Similarity 44.58; Pred. No. 2.3e-13;
Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

QY 724 CGTACAACTTCACGGGCTGCAGCCTTTTACAGATATGTCATGCTGCGATGCGG 783
DB 1775 CATTCACTGTCACAGACCTTAACCTTTTACAGATATGTCATGCTGCGATGCGG 1834
QY 784 TCAAGAGTCAAG---TTCTGAGTGAAGTGCAGCCCAAGAAAATGGGAATGAGT 840
DB 1835 AGGAAGATGTAAGGAGTACTGAGTGAAGTGAAGGAGGAGGAGTGAAGTGAAG 1894
QY 841 AAGAAGTCCATGT---GGCCTGAGACGTGAGAGTCCCAACCAAGCTGAGCGGATG 897
DB 1895 AAGATTAGACCATTAAGCCACCAAGTTTCTGTTAAATATGATCCATCCATCTCAG 1954
QY 898 GAAGAAGGCCAGTGCCTGTTTATGAGAAGGCAAGGAGGAGGAGGAGGAGGAGGAG 957
DB 1955 GCTACAGACCTGACACTGCTGGAAGACATTTGCCCTTTTGAAGCCATGGAAGAA 2014
QY 958 CACTTGGCTACACATATGCTACTATCCAGAACCAACTACCTACAGAAACATGA 1017
DB 2015 TCTTGATTTATGAAGTACTCTCAAGATGAATCAATTTCAAAATTTACACAGTTA 2074
QY 1018 ACATCTAACCCAGCTTGAAGTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1077
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DB 2189 TTCAAGTACTACCTCTGATGATGATCTTAAAGCATTTCCCAAGATTAACATCTTTGGG 2248
QY 1198 TGAAGTGAAGCTGCTGCTAGAGTGAAGCACTTGGATGATGATGATGATGATG 1257
DB 2249 TGAATGAGTACTCTCAAGGAAATCTTAAGAAATATATCTGAGTGGTGTAT 2308
QY 1258 TGAAGTGAAGCCACCACTCTTCTGGAATCTGCTCAGGCCAGCAAGTGAAG 1317
DB 2309 CAGATTAAGCACTCTGATCAGAGTGGCAACAAGAAATGATGATGATGATGATG 2368
QY 1318 TCCAGCAAGATTAATTAACCTTTCTGCTATTAACATCTCTGCTATCTCAATG 1377
DB 2369 ATTTAAGAGGAACTTGAAGAGCAAAATCTTGTATTAAGTAACTTCACTATATG 2428
QY 1378 ATGCAAGATTTGGGAGCCATATTCATCCAGGCTTATGCCAAGAGGCGTTCATCAG 1437
DB 2429 CTGATGAGCAAGAGCCCTGAATCCATTAAGGATACCTTTAAACAAGCTCACTTCCA 2488
QY 1438 AAGTCTCTGAGACCAAGGTGAGAACTTGGCTGAAGAGGCTCAGATCAATGGAAG 1497
DB 2489 AAGGACCTACTGTCGAGCAAAAAGTAAGGAAAGAAAGGAGGAGTCTAGAGTGGACC 2548
QY 1498 AGATTCCCAAGAGTGAAGAAAGGATCATCTGCAACTACCATCTTTTACCAACTG 1557
DB 2549 AACTTCTGTTGATGATCAGAAATGATTTTACAGAAATTAATATTTTATTAAGAACCA 2608
QY 1558 AAGTGAAGAAAGATTTCTCAAGACAGTCAATTCACAGATCTTGCAGTGGCGTGGAGT 1617
DB 2609 TCATTGGAATGAAGTCTGCTGATGATGATGATTTTCCACAGAAATATATCATTTGCT 2668
QY 1618 CCTTGAAGCAAGACCTCTTACATTTGCAAGTCAAGGAGGAGGAGGAGGAGGAGGAG 1677
DB 2669 CTTTGAAGTGAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 2728
QY 1678 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1705

DB 2729 AGGATGCTCAGAAATCACTTTTACTTAC 2756

RESULT 15

US-09-313-942-23
Sequence 23, Application US/09313942
Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25
SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 23
LENGTH: 3507

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS
LOCATION: (1)...(3504)

US-09-313-942-23

Query Match 3.28; Score 76.4; DB 4; Length 3507;
Best Local Similarity 44.58; Pred. No. 2.3e-13;
Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

QY 724 CGTACAACTTCACGGGCTGCAGCCTTTTACAGATATGTCATGCTGCGATGCGG 783
DB 1805 CATTCACTGTCACAGACCTTAACCTTTTACAGATATGTCATGCTGCGATGCGG 1864
QY 784 TCAAGAGTCAAG---TTCTGAGTGAAGTGCAGCCCAAGAAAATGGGAATGAGT 840
DB 1865 AGGAAGATGTAAGGAGTACTGAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAG 1924
QY 841 AAGAAGTCCATGT---GGCCTGGAAGTGTGAGAGTCTGGAACCAAGCTGAGCGGATG 897
DB 1925 AAGATTAGACCATTAAGCAAGCAAGGATTTCTGTTAAATATGATCCATCTCAG 1984
QY 898 GAAGAAGGCCAGTGCCTGTTTATGAGAAGGCAAGGAGGAGGAGGAGGAGGAGGAG 957
DB 1985 GCTACAGACCTGACACTGCTGAGGAGCAACATTTGCTTTTGAAGCCAAATGGA 2044
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QY 1018 AACTTACTTAACAGACCTTGAAGTGCATCTGGAGGAGGAGGAGGAGGAGGAGGAG 1077
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QY 1378 ATGACAAAGTTGGCGAGCCATATTCATCCAGGCTTATGCGAAAGAGGGGTTCCATCAG 1437
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Db 2459 CTGATGGACCGAGAGCCCTGAAATCCATTAAGGCATACCTTAACAAGCTCCACCTTCCA 2518
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Db 2699 CTTTGACTAGTGACATGTTGTACATGTTAGAAATGGCAGCATACAGATGAAGGTGGA 2758
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Job time : 145 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-892-949-1
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Sequence: 1 ggcacgaggtgtgtgtgcag.....atgagccctcgaggccctca 2402

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2879534

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2258.6	94.0	2480	11	US-09-972-708-3	Sequence 3, App1
3	2225.6	92.7	2238	11	US-09-972-708-5	Sequence 5, App1
4	2075	86.4	2529	11	US-09-892-949-45	Sequence 45, App1
5	1947	81.1	2119	14	US-10-006-265-16	Sequence 16, App1
6	1945.4	81.0	2903	11	US-09-892-949-53	Sequence 53, App1
7	1932.8	80.5	2969	14	US-10-006-265-1	Sequence 1, App1
8	1592.2	66.3	2136	11	US-09-892-949-4	Sequence 4, App1
9	1586.8	66.1	2295	11	US-09-892-949-68	Sequence 68, App1
10	1586.4	65.3	2445	14	US-10-227-884-91	Sequence 91, App1
11	1586.4	65.3	2445	14	US-10-230-163-91	Sequence 91, App1
12	1586.4	65.3	2445	14	US-10-230-338-91	Sequence 91, App1
13	1586.4	65.3	2445	14	US-10-218-631-91	Sequence 91, App1
14	1586.4	65.3	2445	14	US-10-230-414-91	Sequence 91, App1
15	1586.4	65.3	2445	14	US-10-216-159A-91	Sequence 91, App1
16	1586.4	65.3	2445	14	US-10-218-849-91	Sequence 91, App1

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18	1568.4	65.3	2445	14	US-10-227-883-91	Sequence 91, Appl
19	1568.4	65.3	2445	14	US-10-219-076-91	Sequence 91, Appl
20	1568.4	65.3	2445	14	US-10-230-434-91	Sequence 91, Appl
21	1568.4	65.3	2445	14	US-10-219-003-91	Sequence 91, Appl
22	1568.4	65.3	2445	14	US-10-219-075-91	Sequence 91, Appl
23	1568.4	65.3	2445	14	US-10-219-464-91	Sequence 91, Appl
24	1568.4	65.3	2445	14	US-10-219-466-91	Sequence 91, Appl
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28	1568.4	65.3	2445	14	US-10-232-231-91	Sequence 91, Appl
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43	1568.4	65.3	2445	14	US-10-227-882-91	Sequence 91, Appl
44	1568.4	65.3	2445	14	US-10-230-436-91	Sequence 91, Appl
45	1568.4	65.3	2445	14	US-10-232-223-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-892-949-1
Sequence 1, Application US/09892949
Publication No. US2003096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuifer, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OR INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2402
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (171)...(2366)
US-09-892-949-1

Query Match 100.0%; Score 2402; DB 11; Length 2402;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGCACGAGGTGTGTGTGCATATGAANTTAGACAGGACGAGTGTACCTTGTTC 60

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DB 121 AATGTCCGCAAAACATTTCTCTCTCCAGCCTTCAATGTGTTAACCTGGGGATGATGTGA 180
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DB 181 CCTGGGCACTGTGATGTCTCCCTCAGCTGCAATTTAGGCTGGGAGCTGTCCAGCTA 240
OY 241 AGCCTGAGAACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 AGCCTGAGAACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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RESULT 2
US-09-972-708-3
Sequence 3, Application US/09972708
Publication No. US20030059871A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Willey, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972.708
NUMBER OF FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 2480
TYPE: DNA
ORGANISM: Homo sapiens
US-09-972-708-3
Query Match 94.0%; Score 2258.6; DB 11; Length 2480;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2261; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY	1338	CCTTTCTGGTGCATAACATCTCTGTATTCAAATGTTGCATGACAAAGTTGGCGAGCA	1397
Db	1207	CCTTTCTGGTGCATAACATCTCTGTATTCAAATGTTGCATGACAAAGTTGGCGAGCA	1286
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QY	1578	AAGACATGCATTCACAGATCTTCACATAGCGGCTGGAGTCCCGAAAAAGAAACACCTC	1637
Db	1447	AAGACATGCATTCACAGATCTTCACATAGCGGCTGGAGTCCCGAAAAAGAAACACCTC	1506
QY	1638	TACATTTGTCAGTATGAGCCAGCAGCAGTCTGGGGAAACCAACGGGACCCAGATTAAT	1697
Db	1507	TACATTTGTCAGTATGAGCCAGCAGCAGTCTGGGGAAACCAACGGGACCCAGATTAAT	1566
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QY	1878	GGAGATGATTTCAAGGATTAAGCTAAAGCTGAAGAGTCTGATGACTCTGTATACACAGAA	1937
Db	1747	GGAGATGATTTCAAGGATTAAGCTAAAGCTGAAGAGTCTGATGACTCTGTATACACAGAA	1806
QY	1938	GACAGGATCTTTAAACCATGTTCCACCCCGACAGTACAAAGTTGGGATTTGACAAGTTGGTG	1997
Db	1807	GACAGGATCTTTAAACCATGTTCCACCCCGACAGTACAAAGTTGGGATTTGACAAGTTGGTG	1866
QY	1998	GTTGACCTTTGGGAATGTTCTGCAAGAAATTTTCCACAGATGAAGCCAGAACGGGTACAGGAA	2057
Db	1867	GTTGACCTTTGGGAATGTTCTGCAAGAAATTTTCCACAGATGAAGCCAGAACGGGTACAGGAA	1926
QY	2058	AACATATTTAGAGGGGAAAAAAGATGGGATTTGACCTGCCCCCTTACAGCCTGATTTGCC	2117
Db	1927	AACATATTTAGAGGGGAAAAAAGATGGGATTTGACCTGCCCCCTTACAGCCTGATTTGCC	1986
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RESULT 4			
US-09-892-949-45			
: Sequence 45, Application US/09892949			
: Publication No. US20030096339A1			
: GENERAL INFORMATION:			
: APPLICANT: Sprecher, Cindy A.			
: APPLICANT: Presnell, Scott R.			
: APPLICANT: Gao, Zeren			
: APPLICANT: Whitmore, Theodore E.			
: APPLICANT: Kuiper, Joseph L.			
: APPLICANT: Maier, Mark F.			
: TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17			
: FILE REFERENCE: 00-42			
: CURRENT APPLICATION NUMBER: US/09/892,949			
: CURRENT FILING DATE: 2001-06-26			
: PRIOR APPLICATION NUMBER: US 60/214,282			
: PRIOR FILING DATE: 2000-06-26			
: PRIOR APPLICATION NUMBER: US 60/214,955			
: PRIOR FILING DATE: 2000-06-29			
: PRIOR APPLICATION NUMBER: US 60/267,963			
: PRIOR FILING DATE: 2001-08-02			
: NUMBER OF SEQ ID NOS: 93			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 45			
: LENGTH: 2529			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (162)...(2108)			
US-09-892-949-45			
Query Match 86.4%; Score 2075; DB 11; Length 2529;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2075; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
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Db	1	TGTGTGTGCAGATGTAATAAATTGAGCAGGAAGGAGAGTGTAGCTTGTTCACCTCAC	60
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Qy	130	AAACATTTCTCTTCCCAAGCCTTATGTGTTAACTTGGGGATGATGTGAGCTTGGGCAC	189
Db	121	AAACATTTCTCTTCCCAAGCCTTATGTGTTAACTTGGGGATGATGTGAGCTTGGGCAC	180
Qy	190	TGTGATCTCTCCCTCACCTCTGCAAAATTCAGCTGGCAGCTTGGCAGCTAAGCCTGGAGA	249
Db	181	TGTGATCTCTCCCTCACCTCTGCAAAATTCAGCTGGCAGCTTGGCAGCTAAGCCTGGAGA	240
Qy	250	ACATTTCTGTGTCTACTACTATAGAAAAAATTTAACTGCACCTGGAGTCCAGGAAGG	309
Db	241	ACATTTCTGTGTCTACTACTATAGAAAAAATTTAACTGCACCTGGAGTCCAGGAAGG	300
Qy	310	AAACAGTTATACCCAGTACACAGTTAAGAGAACTTACCGCTTTTGAGAAAAACATGATA	369
Db	301	AAACAGTTATACCCAGTACACAGTTAAGAGAACTTACCGCTTTTGAGAAAAACATGATA	360
Qy	370	ATTGTACACCAATAGTTCTACAGTGAAGAAACGTGCTTCGTGCTTTTTCCTTCGAA	429

361 ATGTACACCAATAGTTCTACAGTGAATTCGTCTGTCCTTTTCCCTCCAA 420
430 GAATACGATCCAGATATATTATACATTTGAGGTGAAGCTGAATAAGAGATGTGTA 489
421 GAATACGATCCAGATATATTATACATTTGAGGTGAAGCTGAATAAGAGATGTGTA 480
490 TTAATCTCATATGACATAGTGAAGATTAGAGAACATAGCGAAAACTGACCACTAGA 549
481 TTAATCTCATATGACATAGTGAAGATTAGAGAACATAGCGAAAACTGACCACTAGA 540
550 TTTTCCCTGTGAACCACTTTTGGGATCAACCAATATTCCTTAATTTGAATGATAAGC 609
541 TTTTCCCTGTGAACCACTTTTGGGATCAACCAATATTCCTTAATTTGAATGATAAGC 600
610 CTGAGTTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACA 669
601 CTGAGTTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACA 660
670 GTACAGCTGATGGAAGTCACTTCGCTAGAAACCCGTAAGGATTAACCAACGCTACA 729
661 GTACAGCTGATGGAAGTCACTTCGCTAGAAACCCGTAAGGATTAACCAACGCTACA 720
730 ACCTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGCGGTCAGG 789
721 ACCTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGCGGTCAGG 780
790 AGTCAAAGTTCGAGTACTGAGTGAAGCCAAAGAAAAATGGAATGACTAGGAAAGAGCTC 849
781 AGTCAAAGTTCGAGTACTGAGTGAAGCCAAAGAAAAATGGAATGACTAGGAAAGAGCTC 840
850 CATGTGGCTGGAACCTGTGAGAGTCTGAAACCAAGCTGAGCGGATGGAAGAGCCAG 909
841 CATGTGGCTGGAACCTGTGAGAGTCTGAAACCAAGCTGAGCGGATGGAAGAGCCAG 900
910 TGGGTTGTATNGAAGAGGCAAGAGAGGCCCAAGTCTGAGAGAAACACTTGGCTACA 969
901 TGGGTTGTATNGAAGAGGCAAGAGAGGCCCAAGTCTGAGAGAAACACTTGGCTACA 960
970 ACATATGCTACTATCCAGAAAGCAACACTAACCTCACAGAAACATGAACTACTAAC 1029
961 ACATATGCTACTATCCAGAAAGCAACACTAACCTCACAGAAACATGAACTACTAAC 1020
1030 AGCAGCTTGAACCTGATCTGGGAGGCGCAGAGCTTTGGGTCTATGATTTCTTATTA 1089
1021 AGCAGCTTGAACCTGATCTGGGAGGCGCAGAGCTTTGGGTCTATGATTTCTTATTA 1080
1090 CTCTGGGAAGTCCAGTGGCCAGCCCTGAGGATTCGAGTATTCAGAAAAATCATATTC 1149
1081 CTCTGGGAAGTCCAGTGGCCAGCCCTGAGGATTCGAGTATTCAGAAAAATCATATTC 1140
1150 AGTCATTTGAGTATGACAGGCTGCTGCTGAGAGACAGCTAGTGTGAAGTGGCAAA 1209
1141 AGTCATTTGAGTATGACAGGCTGCTGCTGAGAGACAGCTAGTGTGAAGTGGCAAA 1200
1210 GCTTGTCTAGACGTGAACACTTTGATGATTAATGTTCCGAGTGTGACATCAGAGC 1269
1201 GCTTGTCTAGACGTGAACACTTTGATGATTAATGTTCCGAGTGTGACATCAGAGC 1260
1270 CCACACCCCTTCTCGGGAATCTGTCGTCAGGCCACGACACTGACGATCCAGAGATA 1329
1261 CCACACCCCTTCTCGGGAATCTGTCGTCAGGCCACGACACTGACGATCCAGAGATA 1320
1330 AATTAAAACTTTCTGTGCTATTAACATCTCTGTATCCAAATGTTGATGACAAAGTTG 1389
1321 AATTAAAACTTTCTGTGCTATTAACATCTCTGTATCCAAATGTTGATGACAAAGTTG 1380
1390 GCGAGCCATATTCATCCAGGCTTATGCGCAAGAGGCTTCATCAGAGGCTCTGAGA 1449
1381 GCGAGCCATATTCATCCAGGCTTATGCGCAAGAGGCTTCATCAGAGGCTCTGAGA 1440
1450 CCAAGGTGAGAAACATTTGGCTGAAAGAGGTCACGATACATGGAAGAGATTCACAGA 1509
1441 CCAAGGTGAGAAACATTTGGCTGAAAGAGGTCACGATACATGGAAGAGATTCACAGA 1500

1510 GTGAGAGAAAGGCTATCATCTGCAACACTACACATCTTTTACCAAGCTGAAGTGAAGA 1569
1501 GTGAGAGAAAGGCTATCATCTGCAACACTACACATCTTTTACCAAGCTGAAGTGAAGA 1560
1570 GATTCTCCAGACACTCAATTCACGATCTTGACATAGCGGCTGAGTCCCTGAACGAA 1629
1561 GATTCTCCAGACACTCAATTCACGATCTTGACATAGCGGCTGAGTCCCTGAACGAA 1620
1630 AGACCTTTACATTTTTCAGGTCATGCGCCAGCAGCAGAGTGTGGGGAACCAACGGGACA 1689
1621 AGACCTTTACATTTTTCAGGTCATGCGCCAGCAGCAGAGTGTGGGGAACCAACGGGACA 1680
1690 GCATTAATTTTCAGACATTTGTCATGAGTGTGAGATTAATCTCATTAACCTCTGTA 1749
1681 GCATTAATTTTCAGACATTTGTCATGAGTGTGAGATTAATCTCATTAACCTCTGTA 1740
1750 TTGTTGAGGCTCTTATTCATTAATCTGACAGTGGAGATATGTTCAAAAAACCCA 1809
1741 TTGTTGAGGCTCTTATTCATTAATCTGACAGTGGAGATATGTTCAAAAAACCCA 1800
1810 ACAATTTACTCATCTGTGTTGGCCACCCTTTCCCAACCTGCTGAAAGTATATAGCA 1869
1801 ACAATTTACTCATCTGTGTTGGCCACCCTTTCCCAACCTGCTGAAAGTATATAGCA 1860
1870 CATGCGATGAGATGATTTCAAGATAGCTAAACCTGAAGAGTCTGATGACTCTGTGA 1929
1861 CATGCGATGAGATGATTTCAAGATAGCTAAACCTGAAGAGTCTGATGACTCTGTGA 1920
1930 ACACAGAGACAGATCTTAAACCATGTTCCACCCCAAGTGAACAGTGTGATTTGACA 1989
1921 ACACAGAGACAGATCTTAAACCATGTTCCACCCCAAGTGAACAGTGTGATTTGACA 1980
1990 AGTTGCTGTGACCTTGGGATGTTTGCAGAAATTTTTCAGATGATAAGCCGGAAGG 2049
1981 AGTTGCTGTGACCTTGGGATGTTTGCAGAAATTTTTCAGATGATAAGCCGGAAGG 2040
2050 GTCAAGAAACAAATTTAGAGGCGGAAAAAGATGGG 2084
2041 GTCAAGAAACAAATTTAGAGGCGGAAAAAGATGGG 2075

RESULT 5
US-10-006-265-16
: Sequence 16, Application US/10006265
: Publication No. US20030125520A1
: GENERAL INFORMATION:
: APPLICANT: Maeda, Masatsugu
: TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
: FILE REFERENCE: 06501-096001
: CURRENT APPLICATION NUMBER: US/10-006-265
: PRIOR FILING DATE: 2003-01-06
: PRIOR APPLICATION NUMBER: PCT/JP00/03556
: PRIOR FILING DATE: 2000-06-01
: PRIOR APPLICATION NUMBER: JP 11/155797
: PRIOR FILING DATE: 1999-06-02
: PRIOR APPLICATION NUMBER: JP 11/217797
: PRIOR FILING DATE: 1999-07-30
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 16
: LENGTH: 2119
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (11)...(1996)
US-10-006-265-16

Query Match 81.1%; Score 1947; DB 14; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	138	CTCTCTCCCAAGCCTTATGTTTAACCTGGGATGATGTGGACCTGGGACACTGTSATG	197
Db	17	CTCTCTCCCAAGCCTTATGTTTAACCTGGGATGATGTGGACCTGGGACACTGTSATG	76
OY	198	CTCCCTCACCTCTCAATTCAGCCTGGAGCTGTGGCAGCTAAGCCTGGAACATTTCC	257
Db	77	CTCCCTCACCTCTCAATTCAGCCTGGAGCTGTGGCAGCTAAGCCTGGAACATTTCC	136
OY	258	TGTGTCTACTACTATAGGAAAATTTAACCCTGCACCTTGGAGCTCCAGAAAGAACCACT	317
Db	137	TGTGTCTACTACTATAGGAAAATTTAACCCTGCACCTTGGAGCTCCAGAAAGAACCACT	196
OY	318	TATACCCAGTACACAGTTAAGAGAACTTTAGCCTTTTGGAGAAAACATGATTAATTGACA	377
Db	197	TATACCCAGTACACAGTTAAGAGAACTTTAGCCTTTTGGAGAAAACATGATTAATTGACA	256
OY	378	ACCAATAGTCTACAGTGAATAATCGTCTCGTCTCTTTTCCTTCCAAGAAATAGC	437
Db	257	ACCAATAGTCTACAGTGAATAATCGTCTCGTCTCTTTTCCTTCCAAGAAATAGC	316
OY	438	ATCCACAGTAAATTATACCATTTAGCTGGGAAGCTGAATAAGAGATGGTATTAATTAATCT	497
Db	317	ATCCACAGTAAATTATACCATTTAGCTGGGAAGCTGAATAAGAGATGGTATTAATTAATCT	376
OY	498	CATATGACATTAAGAGATTAAGAGACATAGCGAAAACTGAAACCCACTAAGATTTCCGT	557
Db	377	CATATGACATTAAGAGATTAAGAGACATAGCGAAAACTGAAACCCACTAAGATTTCCGT	436
OY	558	GTGAACACAGTTTGGGCACTCAACCAATGATTTAAATTGAATGGATTAAGCCTGAGTTG	617
Db	437	GTGAACACAGTTTGGGCACTCAACCAATGATTTAAATTGAATGGATTAAGCCTGAGTTG	496
OY	618	GCGCCTGTTTCATGTGATTTAAATAACACTTGCATTCAGGACAGTCAACAGTACGAGC	677
Db	497	GCGCCTGTTTCATGTGATTTAAATAACACTTGCATTCAGGACAGTCAACAGTACGAGC	556
OY	678	TGATGGAAGTCAACTTCGCTAGAACCCGTAAGATTAATAACCAAGCTACACCTCAGC	737
Db	557	TGATGGAAGTCAACTTCGCTAGAACCCGTAAGATTAATAACCAAGCTACACCTCAGC	616
OY	738	GGCGTGCAGCCTTTTACAGAAATATGATACCTTCGGATGTGGGGTCAAGAGATTCAAAG	797
Db	617	GGCGTGCAGCCTTTTACAGAAATATGATACCTTCGGATGTGGGGTCAAGAGATTCAAAG	676
OY	798	TTCTGAGTGACTGTGAGCCCAAGAAAATATGGGAATGACTGAGAAAGAGCTCCATGTGGC	857
Db	677	TTCTGAGTGACTGTGAGCCCAAGAAAATATGGGAATGACTGAGAAAGAGCTCCATGTGGC	736
OY	858	CTGGAACCTGTGAGAGTCTGTAACCAAGCTGAGCGGATGGGAAGAAGCCAGTCCGGTTG	917
Db	737	CTGGAACCTGTGAGAGTCTGTAACCAAGCTGAGCGGATGGGAAGAAGCCAGTCCGGTTG	796
OY	918	TTATGGAAGAAAGGAGAGAGCCCAAGTCTTAAGAAAACACTTGGCTACAAACATATAGG	977
Db	797	TTATGGAAGAAAGGAGAGAGCCCAAGTCTTAAGAAAACACTTGGCTACAAACATATAGG	856
OY	978	TACTATCCAGAAACACACACTTAACCTCAGAGAAACATGAACACTACTAACGACAGTT	1037
Db	857	TACTATCCAGAAACACACACTTAACCTCAGAGAAACATGAACACTACTAACGACAGTT	916
OY	1038	GAAGTGCATCTGGGAGGAGAGCTTTTGGGTGATCTATGATTTCTTAAATTCCTTGGG	1097
Db	917	GAAGTGCATCTGGGAGGAGAGCTTTTGGGTGATCTATGATTTCTTAAATTCCTTGGG	976
OY	1098	AAGTCTCCAGTGGCCACCCTGAGGATTCACGCTATTCAGAAAAATCATTTCACTGCAATT	1157
Db	977	AAGTCTCCAGTGGCCACCCTGAGGATTCACGCTATTCAGAAAAATCATTTCACTGCAATT	1036
OY	1158	GAGGTCAATGACAGGCGCTGCGTTGTGAGAGACAGCTAGTGGTGAAGTGGCAAGCTGCTCT	1217
Db	1037	GAGGTCAATGACAGGCGCTGCGTTGTGAGAGACAGCTAGTGGTGAAGTGGCAAGCTGCTCT	1096

QY	1218	TTACACGGGAACACTTGGATGATTTGANTGGTTTCCGANTGGATCTGACGACCACACC	1277
Db	1097	CTACACGGGAACACTTGGATGATTTGANTGGTTTCCGANTGGATCTGACGACCACACC	1156
QY	1278	CTTTCCTGGGAAATCTGTGCTCAGGCCCCAGNACTGAGCATCCAGCAAGATTAATTTAAA	1337
Db	1157	CTTTCCTGGGAAATCTGTGCTCAGGCCCCAGNACTGAGCATCCAGCAAGATTAATTTAAA	1216
QY	1338	CCTTTCTGGTCTCTTAACATCTCTGTGTATCCAAATGTTGCATGACAAAGTTGGCGAGCCA	1397
Db	1217	CCTTTCTGGTCTCTTAACATCTCTGTGTATCCAAATGTTGCATGACAAAGTTGGCGAGCCA	1276
QY	1398	TATTCATCCACGGCTTATGCCAAGAAGGGCTTCCATCAGAAAGGTCCGTGAGCCAAAGTG	1457
Db	1277	TATTCATCCACGGCTTATGCCAAGAAGGGCTTCCATCAGAAAGGTCCGTGAGCCAAAGTG	1336
QY	1458	GAGAACATTGGCGTGGAAGACGGTCCAGATCCATGAAAGAGATTTCCCAAGAGTAGAGAGA	1517
Db	1337	GAGAACATTGGCGTGGAAGACGGTCCAGATCCATGAAAGAGATTTCCCAAGAGTAGAGAGA	1396
QY	1518	AAGGGTATCATCTGCACTACACTACCATCTTTTACCACGCTGAAGGTGGAAAAAGATTCTCC	1577
Db	1397	AAGGGTATCATCTGCACTACACTACCATCTTTTACCACGCTGAAGGTGGAAAAAGATTCTCC	1456
QY	1578	AAGACAGTCAATTCGACGACATCTTTCAGTACGGCTGGAGTCCCTGAAACGAAAGACCTCT	1637
Db	1457	AAGACAGTCAATTCGACGACATCTTTCAGTACGGCTGGAGTCCCTGAAACGAAAGACCTCT	1516
QY	1638	TACATTTGTCAGGTCATATGCCCCAGCACCAAGTCTTGGGGAAACCAACGGGACCAGCATTAAT	1697
Db	1517	TACATTTGTCAGGTCATATGCCCCAGCACCAAGTCTTGGGGAAACCAACGGGACCAGCATTAAT	1576
QY	1698	TTCAAGACATTGCTATTCAGTGTCTTTGAGATTTATCCCATACCTTCTCGATTGGTGGGA	1757
Db	1577	TTCAAGACATTGCTATTCAGTGTCTTTGAGATTTATCCCATACCTTCTCGATTGGTGGGA	1636
QY	1758	GGCCTCTTATTTCTCATTTATTCCTGACAGTGGCATATGCTCTCAAAAAACCCACAATTTG	1817
Db	1637	GGCCTCTTATTTCTCATTTATTCCTGACAGTGGCATATGCTCTCAAAAAACCCACAATTTG	1696
QY	1818	ACTCATCTGTTTGGCCCCACGGTCCCAACCCCTGCTGAAATAGTATATAGCCACATGGGCAT	1877
Db	1637	ACTCATCTGTTTGGCCCCACGGTCCCAACCCCTGCTGAAATAGTATATAGCCACATGGGCAT	1756
QY	1878	GGAGATGATTTTCAAGGATTAAGCTTAACCTGAAGAGTCTGATGACTCTGTGAACACAGAA	1937
Db	1757	GGAGATGATTTTCAAGGATTAAGCTTAACCTGAAGAGTCTGATGACTCTGTGAACACAGAA	1816
QY	1938	GACAGGATCTTAAANCAATGTTTCCACCCCGTAGTACAAAGTTGGTGATTTGACAAATTTG	1997
Db	1817	GACAGGATCTTAAANCAATGTTTCCACCCCGTAGTACAAAGTTGGTGATTTGACAAATTTG	1876
QY	1998	GTGAACCTTTGGGAATGTTCTCCAGAGAAATTTTCCAGATGAAAGCCAAACGGGTACAGAA	2057
Db	1877	GTGAACCTTTGGGAATGTTCTCCAGAGAAATTTTCCAGATGAAAGCCAAACGGGTACAGAA	1936
QY	2058	AACCAATTTAGCAGGGGAAAGCAATGGC 2084	
Db	1937	AACCAATTTAGCAGGGGAAAGCAATGGC 1963	

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US-09-892-949-53
: RESULT 6
: Sequence 53, Application US/09892949
: Publication No. US2003096339A1
: GENERAL INFORMATION:
: APPLICANT: Sprecher, Cindy A.
: APPLICANT: Presnell, Scott R.
: APPLICANT: Gao, Zeren
: APPLICANT: Whitmore, Theodore E.
: APPLICANT: Kuljper, Joseph L.
: APPLICANT: Maurer, Mark F.
: TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17

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: FILE REFERENCE: 00-42
: CURRENT APPLICATION NUMBER: US/09/892,949
: CURRENT FILING DATE: 2001-06-26
: PRIOR APPLICATION NUMBER: US 60/214,282
: PRIOR FILING DATE: 2000-06-26
: PRIOR APPLICATION NUMBER: US 60/214,955
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: US 60/267,963
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 53
: LENGTH: 2903
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (497)...(2482)
: US-09-892-949-53

Query Match      81.0%: Score 1945.4: DB 11: Length 2903:
Best Local Similarity 99.9%: Pred. No. 0:
Matches 1946: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 138 CTCCTCCCGCAGCCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCACTGTGATG 197
    |||
Db 503 CTCCTCCCGCAGCCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCACTGTGATG 562

OY 198 CTCCTCCCGCAGCCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCACTGTGATG 257
    |||
Db 563 CTCCTCCCGCAGCCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCACTGTGATG 622

OY 258 TGTGTCTACTACTATAGAGAAAATTTAACCTGCACCTTGAGTCCAGGAAAAGAACCACT 317
    |||
Db 623 TGTGTCTACTACTATAGAGAAAATTTAACCTGCACCTTGAGTCCAGGAAAAGAACCACT 682

OY 318 TATACCCAGTACACAGCTTAAGAGACCTTTGGAGAGAAAACATGATTAATTGTACA 377
    |||
Db 683 TATACCCAGTACACAGCTTAAGAGACCTTTGGAGAGAAAACATGATTAATTGTACA 742

OY 378 ACCAATAGTCTACAACTGAAAATCGTCTGCTCTTTTCCCTCCAGAAATACG 437
    |||
Db 743 ACCAATAGTCTACAACTGAAAATCGTCTGCTCTTTTCCCTCCAGAAATACG 802

OY 438 ATCCCAATATATTTATACATTGAGTGAAGCTGAATGAGATGGTATTAATTAATCT 497
    |||
Db 803 ATCCCAATATATTTATACATTGAGTGAAGCTGAATGAGATGGTATTAATTAATCT 862

OY 498 CATATGACATATGAGATTAAGAGACATAGCAAAAACCTGAACCACTTAAGATTTCCGT 557
    |||
Db 863 CATATGACATATGAGATTAAGAGACATAGCAAAAACCTGAACCACTTAAGATTTCCGT 922

OY 558 GTGAACACAGTTTGGGCAATCAAGATGTTCAATTTGAATGATTAAGCCGTGATG 617
    |||
Db 923 GTGAACACAGTTTGGGCAATCAAGATGTTCAATTTGAATGATTAAGCCGTGATG 982

OY 618 GCGGCTTTTCATCTGATTTAAATATACACATTCGATTCAGAGACGTCAACAGTACAGC 677
    |||
Db 983 GCGGCTTTTCATCTGATTTAAATATACACATTCGATTCAGAGACGTCAACAGTACAGC 1042

OY 678 TGAATGGAAGTCAACTTCGCTAAGAACCGTAAGATTAAGCAACAGCTCAACCTCAGC 737
    |||
Db 1043 TGAATGGAAGTCAACTTCGCTAAGAACCGTAAGATTAAGCAACAGCTCAACCTCAGC 1102

OY 738 GGGGTGAGGCTTTTACAGATATGTCATAGCTGTGAGATGTGGGTCAGAGGATCAAG 797
    |||
Db 1103 GGGGTGAGGCTTTTACAGATATGTCATAGCTGTGAGATGTGGGTCAGAGGATCAAG 1162

OY 798 TTTCTGAGTACTGAGACCAAGAAAATGGAATGACTGAGAGAAAGCTCCATGTGGC 857
    |||
Db 1163 TTTCTGAGTACTGAGACCAAGAAAATGGAATGACTGAGAGAAAGCTCCATGTGGC 1222

OY 858 CTGGAAGTGTGAGAGTCTTGAAAACAGCTGAGCGGATGGAAGAACGCCAGTGGGTTG 917
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|||
Db 1223 CTGGAAGTGTGAGAGTCTTGAAAACAGCTGAGCGGATGGAAGAACGCCAGTGGGTTG 1282

OY 918 TTATGGAAGAAAGCAAGAGAGAGCCCGACTCTTAAGAAAACACTTGGCTACACATATGG 977
    |||
Db 1283 TTATGGAAGAAAGCAAGAGAGAGCCCGACTCTTAAGAAAACACTTGGCTACACATATGG 1342

OY 978 TACTATCCAGAAACACACTAATCACTCAGAAAACATGTAACACTACTAATCACTGAT 1037
    |||
Db 1343 TACTATCCAGAAACACACTAATCACTCAGAAAACATGTAACACTACTAATCACTGAT 1402

OY 1038 GAATCTGATCTGGAGGCGAGAGAGCTTTGGGTCTATGATTTCTTAAATTCCTTGGG 1097
    |||
Db 1403 GAATCTGATCTGGAGGCGAGAGAGCTTTGGGTCTATGATTTCTTAAATTCCTTGGG 1462

OY 1098 AAGTCTCCAGTGGCGACCCCTGAGGATTCAGACTATTTCAAAAAATATCTTCAGTGAT 1157
    |||
Db 1463 AAGTCTCCAGTGGCGACCCCTGAGGATTCAGACTATTTCAAAAAATATCTTCAGTGAT 1522

OY 1158 GAGGTCAATGAGGCGCTCGTTGCTGAGAGACAGCTAGTGGTAAGTGCACAAGCTCTGCT 1217
    |||
Db 1523 GAGGTCAATGAGGCGCTCGTTGCTGAGAGACAGCTAGTGGTAAGTGCACAAGCTCTGCT 1582

OY 1218 CTAGACGTGAACACCTTGGATGATTAATGATGTTCCGAGATGAGACTGAGGCCACCACC 1277
    |||
Db 1583 CTAGACGTGAACACCTTGGATGATTAATGATGTTCCGAGATGAGACTGAGGCCACCACC 1642

OY 1278 CTTTCCCTGGGAATCTGTGTCTCAGGCCACCAACACTGAGACATCCAGAAAGATTAATTA 1337
    |||
Db 1643 CTTTCCCTGGGAATCTGTGTCTCAGGCCACCAACACTGAGACATCCAGAAAGATTAATTA 1702

OY 1338 CTTTCTGTGTCTATACATCTGTGTATTCATCATTTGTGATGACAAAGTTGGGAGCCA 1397
    |||
Db 1703 CTTTCTGTGTCTATACATCTGTGTATTCATCATTTGTGATGACAAAGTTGGGAGCCA 1762

OY 1398 TATTCCATCCAGGCTTAATGCCAAAAGGCGTTCCATAGAGAGTCTTGAGACCAGGTG 1457
    |||
Db 1763 TATTCCATCCAGGCTTAATGCCAAAAGGCGTTCCATAGAGAGTCTTGAGACCAGGTG 1822

OY 1458 GAGAACATTTGGCGGAGAGAGGCTGACATGATCAATGGAAGAAAGATTTCCAGAGTGAAGA 1517
    |||
Db 1823 GAGAACATTTGGCGGAGAGAGGCTGACATGATCAATGGAAGAAAGATTTCCAGAGTGAAGA 1882

OY 1518 AAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAGAAAGATTCTCC 1577
    |||
Db 1883 AAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAGAAAGATTCTCC 1942

OY 1578 AAGCACTCAATTCACACATCTTGCACTACGGCTGAGTCCCTGAAACGAAAGACCTCT 1637
    |||
Db 1943 AAGCACTCAATTCACACATCTTGCACTACGGCTGAGTCCCTGAAACGAAAGACCTCT 2002

OY 1638 TACATGTTGAGGTCATGAGGCGAGACAGCAGTGGGGAAGCAAGGGGACACATTAAT 1697
    |||
Db 2003 TACATGTTGAGGTCATGAGGCGAGACAGCAGTGGGGAAGCAAGGGGACACATTAAT 2062

OY 1698 TTCAAGACATTTGATTCAGTCACTGCTTTGAGATTAATCCCTAATACCTCTGATTTGGTGA 1757
    |||
Db 2063 TTCAAGACATTTGATTCAGTCACTGCTTTGAGATTAATCCCTAATACCTCTGATTTGGTGA 2122

OY 1758 GGCCTTTTATTTCTCATTTATCTGACAGTGGCATATGCTCAAAAAAACCAAAATTTG 1817
    |||
Db 2123 GGCCTTTTATTTCTCATTTATCTGACAGTGGCATATGCTCAAAAAAACCAAAATTTG 2182

OY 1818 ACTCATCTGTGTTGGCCACCGTTCGCCAACCGTGAAGTGTATAGCCACATGGCAT 1877
    |||
Db 2183 ACTCATCTGTGTTGGCCACCGTTCGCCAACCGTGTGAAGTGTATAGCCACATGGCAT 2242

OY 1878 GGAAGATATTTCAAGATAAGCTAAGCTGAAGAGTCTGATGACTCTGTGAACACAGAA 1937
    |||
Db 2243 GGAAGATATTTCAAGATAAGCTAAGCTGAAGAGTCTGATGACTCTGTGAACACAGAA 2302

OY 1938 GACAGAGTCTTAAACCATTTCCACCCTCAGTGAACAGTTGGTGAAGTAAGTTGGTG 1997
    |||
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Dc 2303 GACAGGATCTTTAAACCATGTTCCACCCCGAGTGAACAAGTTGGATTTGACAAAGTTGGTG 2362

QY 1998 GTGAACTTTGGGAAATGTTTCGCAGAAATTTTCACATGAAAGCAGAAACGGGTCAGAA 2057

Dd 2363 GTGAACTTTGGGAAATGTTTCGCAGAAATTTTCACAGATGAAGCAGAAACGGGTGAGAA 2422

QY 2058 AACCAATTTAGGAGGCGAAACAGATGGG 2084

Dd 2423 AACCAATTTAGGAGGCGAAACAGATGGG 2449

RESULT 7
US-10-00

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? Sequence 1 Application 10006265
? Publication No. US20030125520A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Maeda, Masatsugu
? APPLICANT: Yaguchi, No. US20030125520A1iko
? TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
? FILE REFERENCE: 06501-096001
?
? CURRENT APPLICATION NUMBER: US/10/006,265
? CURRENT FILING DATE: 2003-01-06
?
? PRIOR APPLICATION NUMBER: PCT/JP00/03556
? PRIOR FILING DATE: 2000-06-01
?
? PRIOR APPLICATION NUMBER: JP 11/155797
? PRIOR FILING DATE: 1999-06-02
?
? PRIOR APPLICATION NUMBER: JP 11/217797
? PRIOR FILING DATE: 1999-07-30
?
? NUMBER OF SEQ ID NOS: 40
?
? SOFTWARE: FastSeq for Windows Version 4.0
?
? SEQ ID NO 1
?
? LENGTH: 2969
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? FEATURE:
?
? NAME/KEY: CDS
?
? LOCATION: (523)...(2478)
?
? US-10-006-265-1

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Query Match	80.5%;	Score 1932.8;	DB 14;	Length 2969;
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Best Local Similarity	99.8%	Pred.No.	0;
Matches 1945: Conservative	0;	Mismatches	2;
		Indels	1;
		Gaps	1;

[illegible][illegible]

Db 1141 TGGACNATHCARGAARAYRNARCCNTTYTGGTYTAAYAAVHMSNGTNTAYCCN 1200
QY 1371 ATGTGATGACAAAGTTGGCGAGCATATTCATCCAGCGTATATGCCAAGAAGCGTT 1430
Db 1201 ATGTTCATGATAYARGNGNGARCCNTATSNATHCARCANTYAGCNAARGAGGNGT 1260
QY 1431 CCATCAAGAGTCCCTGAGACCAAGTGGAGAACATTTGGCTGAAGCGTCCAGATCACA 1490
Db 1261 CCWMSNGARGNGCNGARCNARAGTNGAARAATATHGNTNARACNGTNGACNATHACN 1320
QY 1491 TGGAAAGAGATTCCCAAGAGTGGAGAAAGGATATCATCTGCACTACACCATCTTTAC 1550
Db 1321 TGGAAAGARATTHCCNAARMSNGARMAAGNATHTHTGAYATYACNATHHTYATY 1380
QY 1551 CAAGCTGAAGTGGAAAGATCTCCACAGTCAATTCAGCATCTCCAGCATCTGGAGTACGC 1610
Db 1381 CAGCGNGARGNGNARAGGNTTYWSNAARACNGTNAAYSNMSNATHYNCARTAGGN 1440
QY 1611 CTGAGTCCCTGAAAGAAAGACCTCTTACATGTTCAGGTGATGGCCAGACAGTGT 1670
Db 1441 YTMGARMSNTYNAARMGNARACNMSNTATATHTGTCNARGTNATGGCNSMACNMSGN 1500
QY 1671 GGGGGAACCAACGGGACCAAGCATTAATTCAGACATGTCTCATAGTGTCTTTGAGATT 1730
Db 1501 GGNAGNACNAAYGNGACNMSNATHAAVTTAARACNTYMSNTTYGATYGAATH 1560
QY 1731 ATCCCTATACCTCTGATGTGGAGCGCTCTTATCTCATCTTATCCGACAGTGGCA 1790
Db 1561 ATHTYTNATHACNMSNTTATHGNGGNGVNTYTNATHYTNATHYTNATHYTNATHYTNATH 1620
QY 1791 TATGCTCTCAAAAACCCCAAAATGTACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1850
Db 1621 TAYGNTYTNARARACNMAAYARNTNACATYNTNGYTGCGCNCNCGNCCNAATCCN 1680
QY 1851 GCTGAAGT 1910
Db 1681 GCGARMSNMSNATHGNCNMTGCGAGYGGNAGAYTTAARAGAYTAAAYTAAAYTAAAR 1740
QY 1911 GAGTGTGATGACCTGTGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1970
Db 1741 GARMNSCATYATYNSNGTNAAYACNGARAGATMGNAHTTNAARCCNTGYSMACNCCNWSN 1800
QY 1971 GACAGT 2030
Db 1801 GAVAAARTNGTNTHGAAYARTNGTNGTNAATTTGNGNAYGNTYTNARARATHHTY 1860
QY 2031 ACAGATGAGACCCAGAACGGGTCAAGAAACAAATTTAGAGGGGAAAGAAATGGGTATGT 2090
Db 1861 ACNAGVARGCNCNMGNCNAGCARAAAYAYTNGNGNAGARARAAVGGTAYGTN 1920
QY 2091 ACCTGGCCCTTCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2150
Db 1921 ACNTGTCCNTTYMGNCNGAYTGTCCYTNNGNARSNNTTYGARGRYTNCCGNTWSN 1980
QY 2151 CCTGAGATTCCTGGCCGAGAAATCCCATATCTAGTTCAGAGATCCAGAGAGACCGC 2210
Db 1981 CCGARATHCCNCCNMGNAARMSNCAATAYTINMGNSNMGNTATCCNGARAGNACMGN 2040
QY 2211 CCAAGAACCAAGAGACAGTCTCTCTTTGTGTCAAAGTTAGTACAGATCATCTGTGT 2270
Db 2041 CCGARCCNARARCARARYNTNTTYWSNCGNCAARSNYTNCCNGAYCAVYTTGTG 2100
QY 2271 GAGGAAG 2330
Db 2101 GARGARAGNGCNCNNAAYCCNTAYTNAARAATWSNTNACNCGNMGNGARTTYTNGTN 2160
QY 2331 TCTGAAAACTTCCAGAGACACCAAGGAGAGAGT 2365
Db 2161 WSNGARARARYTNCNNGARCAVACNAARAGNGARGT 2195

RESULT 9
US-09-892-949-68

Sequence 68, Application US/09892949
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kulper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ. ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEO ID NO 68
LENGTH: 2295
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide encoding human zcytor17-Fc4 fusion
NAME/KEY: CDS
LOCATION: (1)...(2295)
US-09-892-949-68
Query Match 66.1%; Score 1586.8; DB 11; Length 2295;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1588; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 138 CTCCTCCCGCAGCGCTTCATGTGTTAACTGGGATGATGTGACCTGGGCACTGTGATG 197
Db 7 CTCCTCCCGCAGCGCTTCATGTGTTAACTGGGATGATGTGACCTGGGCACTGTGATG 66
QY 198 CTCGCCCATCTGTGCAAAATTCAGCGCTGGCAGCTGTGCACTAACTGTGAACATTTCC 257
Db 67 CTCGCCCATCTGTGCAAAATTCAGCGCTGGCAGCTGTGCACTAACTGTGAACATTTCC 126
QY 258 TGTGTCTACTACTATAGAAAATTTAACTGTGACCTGTGAGTGTGAGGAAAGAACAGT 317
Db 127 TGTGTCTACTACTATAGAAAATTTAACTGTGACCTGTGAGTGTGAGGAAAGAACAGT 186
QY 318 TATACCAGTACACAGTTAAGAGAACTTACGTTTGTGAGAAACATGATTAATTGTACA 377
Db 187 TATACCAGTACACAGTTAAGAGAACTTACGTTTGTGAGAAACATGATTAATTGTACA 246
QY 378 ACCAATAGTCTACAACTGAATAATCTGCTTCTGCTCTTTTCTTCCCAAGAATAAGC 437
Db 247 ACCAATAGTCTACAACTGAATAATCTGCTTCTGCTCTTTTCTTCCCAAGAATAAGC 306
QY 438 ATCCAGATATATATACATTTGAGTGTGAGGAGTGAATAATGAGATGATTAATAATCT 457
Db 307 ATCCAGATATATATACATTTGAGTGTGAGGAGTGAATAATGAGATGATTAATAATCT 366
QY 498 CATATGACATACAGGATAGAGACATATGAGCAAACTGAACACCTAAGATTTTCGGT 557
Db 367 CATATGACATACAGGATAGAGACATATGAGCAAACTGAACACCTAAGATTTTCGGT 426
QY 558 GTGAACACAGTTTGGGCACTAAGCAATGATTAATTAATTAATTAATTAATTAATTAAT 617
Db 427 GTGAACACAGTTTGGGCACTAAGCAATGATTAATTAATTAATTAATTAATTAATTAAT 486
QY 618 GCGCTGTTCATCTGATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 677
Db 487 GCGCTGTTCATCTGATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 546
QY 678 TGGATGGAAGTCACTTCGTAAGAACCTTAAGATTAATAATTAATTAATTAATTAATTAAT 737
Db 546 TGGATGGAAGTCACTTCGTAAGAACCTTAAGATTAATAATTAATTAATTAATTAATTAAT

Db 547 TGAATGGAAGTCAACTTCGCTAAGAACCGTAAGATAAAAAACCAACGTAACCTCAGC 606
QY 738 GGGCTGAGCCTTTTACAGATATGTACATCTGCGGATGTGGGTCGAAGAGTCAAG 797
Db 607 GGGCTGAGCCTTTTACAGATATGTACATCTGCGGATGTGGGTCGAAGAGTCAAG 666
QY 798 TTTGAGATGACTGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAGTCAATGTGC 857
Db 667 TTTGAGATGACTGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAGTCAATGTGC 726
QY 858 CTGGAAGTGGAGAGTCTGAACCAAGCTGAGGCGATGGAAGAAGCCAGTGGTGG 917
Db 727 CTGGAAGTGGAGAGTCTGAACCAAGCTGAGGCGATGGAAGAAGCCAGTGGTGG 786
QY 918 TTATGGAAGAAGGAGAGAGCCCAAGTCTAGAGAAAAACACTTGGCTACAAATATAG 977
Db 787 TTATGGAAGAAGGAGAGAGCCCAAGTCTAGAGAAAAACACTTGGCTACAAATATAG 846
QY 978 TACTATCCAGAAACAACTAATACCTCAGAGAAAAATGAACACTACTAACACAGCTT 1037
Db 847 TACTATCCAGAAACAACTAATACCTCAGAGAAAAATGAACACTACTAACACAGCTT 906
QY 1038 GAAGTCAATGAGGAGGAGAGAGCTTTGGGTCTATGATTTCTTAAATCTCTGGG 1097
Db 907 GAAGTCAATGAGGAGGAGAGAGCTTTGGGTCTATGATTTCTTAAATCTCTGGG 966
QY 1098 AAGTCTCAGTGGCAGCCCTGAGGATTCAGACTATTCAGAAAAATCATTTCACTGAT 1157
Db 967 AAGTCTCAGTGGCAGCCCTGAGGATTCAGACTATTCAGAAAAATCATTTCACTGAT 1026
QY 1158 GAGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217
Db 1027 GAGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1086
QY 1218 CTACAGTGAACACTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1277
Db 1087 CTACAGTGAACACTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
QY 1278 CTTTCCTGGAATCTGTCTCAGGCCAGCACTGAGAGATCCAGAAAGATTAATTA 1337
Db 1147 CTTTCCTGGAATCTGTCTCAGGCCAGCACTGAGAGATCCAGAAAGATTAATTA 1206
QY 1338 CTTTCCTGGAATCTGTCTCAGGCCAGCACTGAGAGATCCAGAAAGATTAATTA 1397
Db 1207 CTTTCCTGGAATCTGTCTCAGGCCAGCACTGAGAGATCCAGAAAGATTAATTA 1286
QY 1398 TATTCATCCAGGCTTATGCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1457
Db 1267 TATTCATCCAGGCTTATGCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326
QY 1458 GAGAACATTTGGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1517
Db 1327 GAGAACATTTGGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1386
QY 1518 AAGGATTCATCTGCAACTACCATCTTTTACCAGCTGAGAGTGAAGAGATCTCC 1577
Db 1387 AAGGATTCATCTGCAACTACCATCTTTTACCAGCTGAGAGTGAAGAGATCTCC 1446
QY 1578 AAGACATTCATCTGCAACTACCATCTTTTACCAGCTGAGAGTGAAGAGATCTCC 1637
Db 1447 AAGACATTCATCTGCAACTACCATCTTTTACCAGCTGAGAGTGAAGAGATCTCC 1506
QY 1638 TACATTTTCAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1697
Db 1507 TACATTTTCAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1566
QY 1698 TTCAAGACATTTGATTCAGTGTCTTGGAG 1727
Db 1567 TTCAAGACATTTGATTCAGTGTCTTGGAG 1596

RESULT 10
US-10-227-884-91

Sequence 91, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090651
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER:	60/095916
PRIOR FILING DATE:	1998-08-10
PRIOR APPLICATION NUMBER:	60/096146
PRIOR FILING DATE:	1998-08-11
PRIOR APPLICATION NUMBER:	60/096791
PRIOR FILING DATE:	1998-08-17
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PRIOR APPLICATION NUMBER:	60/098544
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PRIOR APPLICATION NUMBER:	60/099816
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PRIOR APPLICATION NUMBER:	60/100038
PRIOR FILING DATE:	1998-09-11
PRIOR APPLICATION NUMBER:	60/100385
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100390
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100627
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100848
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PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/101477
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PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1998-09-24
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PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/106178
PRIOR FILING DATE:	1998-10-28
PRIOR APPLICATION NUMBER:	60/106248
PRIOR FILING DATE:	1998-10-29
PRIOR APPLICATION NUMBER:	60/106464
PRIOR FILING DATE:	1998-10-30
PRIOR APPLICATION NUMBER:	60/106905
PRIOR FILING DATE:	1998-11-03
PRIOR APPLICATION NUMBER:	60/108787
PRIOR FILING DATE:	1998-11-17
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PRIOR FILING DATE:	1998-12-22
PRIOR APPLICATION NUMBER:	60/113605
PRIOR FILING DATE:	1998-12-23
PRIOR APPLICATION NUMBER:	60/113621
PRIOR FILING DATE:	1998-12-23
PRIOR APPLICATION NUMBER:	60/115558
PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/115555
PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/115733

1	PRIOR FILING DATE: 1999-01-12
2	PRIOR APPLICATION NUMBER: 60/119549
3	PRIOR FILING DATE: 1999-02-10
4	PRIOR APPLICATION NUMBER: 60/123618
5	PRIOR FILING DATE: 1999-03-10
6	PRIOR APPLICATION NUMBER: 60/125259
7	PRIOR FILING DATE: 1999-03-19
8	PRIOR APPLICATION NUMBER: 60/125775
9	PRIOR FILING DATE: 1999-03-23
10	PRIOR APPLICATION NUMBER: 60/126773
11	PRIOR FILING DATE: 1999-03-29
12	PRIOR APPLICATION NUMBER: 60/127867
13	PRIOR FILING DATE: 1999-04-05
14	PRIOR APPLICATION NUMBER: 60/130232
15	PRIOR FILING DATE: 1999-04-21
16	PRIOR APPLICATION NUMBER: 60/131022
17	PRIOR FILING DATE: 1999-04-26
18	PRIOR APPLICATION NUMBER: 60/131270
19	PRIOR FILING DATE: 1999-04-27
20	PRIOR APPLICATION NUMBER: 60/131291
21	PRIOR FILING DATE: 1999-04-27
22	PRIOR APPLICATION NUMBER: 60/131445
23	PRIOR FILING DATE: 1999-04-28
24	PRIOR APPLICATION NUMBER: 60/134287
25	PRIOR FILING DATE: 1999-05-14
26	PRIOR APPLICATION NUMBER: 60/140650
27	PRIOR FILING DATE: 1999-06-22
28	PRIOR APPLICATION NUMBER: 60/140723
29	PRIOR FILING DATE: 1999-06-22
30	PRIOR APPLICATION NUMBER: 60/141037
31	PRIOR FILING DATE: 1999-06-23
32	PRIOR APPLICATION NUMBER: 60/144758
33	PRIOR FILING DATE: 1999-07-20
34	PRIOR APPLICATION NUMBER: 60/145698
35	PRIOR FILING DATE: 1999-07-26
36	PRIOR APPLICATION NUMBER: 60/146222
37	PRIOR FILING DATE: 1999-07-28
38	PRIOR APPLICATION NUMBER: 60/146953
39	PRIOR FILING DATE: 1999-08-03
40	PRIOR APPLICATION NUMBER: 60/149320
41	PRIOR FILING DATE: 1999-08-17
42	PRIOR APPLICATION NUMBER: 60/149638
43	PRIOR FILING DATE: 1999-08-17
44	PRIOR APPLICATION NUMBER: 60/151733
45	PRIOR FILING DATE: 1999-08-31
46	PRIOR APPLICATION NUMBER: 60/164418
47	PRIOR FILING DATE: 1999-11-09
48	PRIOR APPLICATION NUMBER: 60/166361
49	PRIOR FILING DATE: 1999-11-16
50	PRIOR APPLICATION NUMBER: 60/169445
51	PRIOR FILING DATE: 1999-12-07
52	PRIOR APPLICATION NUMBER: 60/169495
53	PRIOR FILING DATE: 1999-12-07
54	PRIOR APPLICATION NUMBER: 60/169835

Query Match	Best Local Match	Similarity	Score	Pred. No. of Matches	Conservative	Indels	Gaps
65.3%	99.3%	1568.4	0	11	0	2445	
1575	1575	0	11	0	0	0	
QY	4	ACGAGGTGTGTGCGATGATAAATTGACACGAGACAGAGTGTACGTTGTTCCAC	63				
DB	122	AAGACATGTGTGTGCGATGATAAATTGACACGAGACAGAGTGTACGTTGTTCCAC	181				
QY	64	CTCAGCTGGGATGTGCATCAGGCACAACTCAAGTTTTCACACGCGATGTGCTTGAAAT	123				
DB	182	CTCAGCTGGGATGTGCATCAGGCACAACTCAAGTTTTCACACGCGATGTGCTTGAAAT	241				
QY	124	GTCGCGAACAATTCCTCTCCCGACGCTCATGTGTTAACTGGGGATGATGGACCT	183				
DB	242	GTCGCGAACAATTCCTCTCTCCCGACGCTCATGTGTTAACTGGGGATGATGGACCT	301				
QY	184	GGGCACTGTGATGCTCCCTCACTCTGCAAAATTCAGCTGGACACTGTGCACGTAAAGC	243				

Db 302 GGGCAGTGTGGATGCTCCCTTCACTCTGCAAAATTCAGCCCTGGCAGCTCTGCCAGCTAAAC 361
Oy 244 CTGAGAACATTTCCCTGTCTACTACTATAGGAAAAATTTAAACCGCAGCTTGGAGTCCAG 303
Db 362 CTGAGAACATTTCCCTGTCTACTACTATAGGAAAAATTTAAACCGCAGCTTGGAGTCCAG 421
Oy 304 GAAAGGAAACAGTTATACCCAGTACACAGTTAAAGAGACCTTACGCTTTTGGAAAAAC 363
Db 422 GAAAGGAAACAGTTATACCCAGTACACAGTTAAAGAGACCTTACGCTTTTGGAAAAAC 481
Oy 364 ATGATTAATTGTACAAACCAATAGTCTCAAGTAAATCGTCTCCGCTCTTTTCC 423
Db 482 ATGATTAATTGTACAAACCAATAGTCTCAAGTAAATCGTCTCCGCTCTTTTCC 541
Oy 424 TTCCAGAAATACGATCCAGATTAATTAATACATTTAGTGGAGCTGAAATGGAGATG 483
Db 542 TTCCAGAAATACGATCCAGATTAATTAATACATTTAGTGGAGCTGAAATGGAGATG 601
Oy 484 GTGTAATTAATTCATATATGACATATCTGGAGATTAGAGACATAGCGAAAACTGAACAC 543
Db 602 GTGTAATTAATTCATATATGACATATCTGGAGATTAGAGACATAGCGAAAACTGAACAC 661
Oy 544 CTAGATTTTCCGTGTGAAACAGTTTGGCATCAACGAATGATTAATTAATGA 603
Db 662 CTAGATTTTCCGTGTGAAACAGTTTGGCATCAACGAATGATTAATTAATGA 721
Oy 604 TAAAGCCTGAGTTGGCCCTGTTTCATCTGATTAATAATACACATTCGATTCAGAGAC 663
Db 722 TAAAGCCTGAGTTGGCCCTGTTTCATCTGATTAATAATTAATTAATTAATTAATTAAT 781
Oy 664 TCAACAGTACAGCTGATGAGTGAAGTCAACTTCGCTAAGAACCGTAAGATTAATAA 723
Db 782 TCAACAGTACAGCTGATGAGTGAAGTCAACTTCGCTAAGAACCGTAAGATTAATAA 841
Oy 724 CGTCAACCTCAGCGGGGCTGAGGCTTTTACAGAAATATGATATGCTGTGAGATGGGG 783
Db 842 CGTCAACCTCAGCGGGGCTGAGGCTTTTACAGAAATATGATATGCTGTGAGATGGGG 901
Oy 784 TCAAGAGTCAAAATTTCTGAGTACTGAGAGCCCAAGAAAAATGGAGATGACTGAGAG 843
Db 902 TCAAGAGTCAAAATTTCTGAGTACTGAGAGCCCAAGAAAAATGGAGATGACTGAGAG 961
Oy 844 AAGCTCCATGTGGCCTGGAATCTGAGAGTCTCTGAACCAAGCTGAGCGGATGAGAGAA 903
Db 962 AAGCTCCATGTGGCCTGGAATCTGAGAGTCTCTGAACCAAGCTGAGCGGATGAGAGAA 1021
Oy 904 GGGCAGTGGGCTTTTATGAAAGAGCAAGAGAGGCCCGCTCTGAGAAAAACACTG 963
Db 1022 GGGCAGTGGGCTTTTATGAAAGAGCAAGAGAGGCCCGCTCTGAGAAAAACACTG 1081
Oy 964 GCTACAAATATGTGTACTATCCAGAAAGCAACACTAACCTCAGAAAAACATGAACACTA 1023
Db 1082 GCTACAAATATGTGTACTATCCAGAAAGCAACACTAACCTCAGAAAAACATGAACACTA 1141
Oy 1024 CTAAACGACAGCTTGAACCTGATCTGGAGGCGAGAGCTTTTGGGTGCTATGATTTCTT 1083
Db 1142 CTAAACGACAGCTTGAACCTGATCTGGAGGCGAGAGCTTTTGGGTGCTATGATTTCTT 1201
Oy 1084 ATAAATTTCTTTGGGAAGTCTCAGTGGCAGCCCTGAGAGATTCAGACTTCAAAAAAT 1143
Db 1202 ATAAATTTCTTTGGGAAGTCTCAGTGGCAGCCCTGAGAGATTCAGACTTCAAAAAAT 1261
Oy 1144 CATTTAGTGCATTTGAGTCTATGAGGCTGCTGCTTGAAGACACAGTATGAGTGAAGT 1203
Db 1262 CATTTAGTGCATTTGAGTCTATGAGGCTGCTGCTTGAAGACACAGTATGAGTGAAGT 1321
Oy 1204 GGCAGAGCTGCTCTGAGAGTGAACCTTGGATGATTAATGATGCTTCCGAGTGTGACT 1263
Db 1322 GGCAGAGCTGCTCTGAGAGTGAACCTTGGATGATTAATGATGCTTCCGAGTGTGACT 1381
Oy 1264 CAGAGCCACACACCTTTCCGGAATCTGCTCAGGCGACAGAACTGAGCATTCAGC 1323
Db 1382 CAGAGCCACACACCTTTCCGGAATCTGCTCAGGCGACAGAACTGAGCATTCAGC 1441

Oy 1324 AAGATTAATTAACCTTTCTGTCCTATTAACATCTGTGTATCCAAATGTTGATGACA 1383
Db 1442 AAGATTAATTAACCTTTCTGTCCTATTAACATCTGTGTATCCAAATGTTGATGACA 1501
Oy 1384 AAGTTGGGAGCCATATTCATCCAGGCTTATGCCAAAGAGGGCTTCATCAGAGCTC 1443
Db 1502 AAGTTGGGAGCCATATTCATCCAGGCTTATGCCAAAGAGGGCTTCATCAGAGCTC 1561
Oy 1444 CTGAGACCAAGCTGAGAGACATTTGGCTGAGAGCGGTACGATCAGATGAAAGATTC 1503
Db 1562 CTGAGACCAAGCTGAGAGACATTTGGCTGAGAGCGGTACGATCAGATGAAAGATTC 1621
Oy 1504 CCAAGAGTGAAGAGGATTCATCTGCAACTACACATCTTTTACCAACCTGAAGCTG 1563
Db 1622 CCAAGAGTGAAGAGGATTCATCTGCAACTACACATCTTTTACCAACCTGAAGCTG 1681
Oy 1564 GAAAGGATTTCTCCAGACAGCTCAAT 1589
Db 1682 GAAAGGATTTCTCCAGACAGCTCAAT 1707

RESULT 11
US-10-230-163-91
; Sequence 91, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230.163
; PRIOR APPLICATION NUMBER: 2002-08-28
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR APPLICATION NUMBER: 60/082804
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; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
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PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.3%; Score 1568.4; DB 14; Length 2445;

Best Local Similarity 99.3%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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OY 4 ACGAGCTGTGTGAGTATGATAAATTGACAGAGAGAGAGTGTGAGTTCAC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 122 AAGCATGTGTGTGAGATGATAAATTGACAGAGAGAGTGTGAGTTCAC 181
OY 64 CTCAGCTGGAGATGTCATCAGGCACTCAAGTTTTCACAGGATGTGTGTGAT 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 182 CTCAGCTGGAGATGTCATCAGGCACTCAAGTTTTCACAGGATGTGTGTGAT 241
OY 124 GTCCGCAAAACATTTCTCTCCCGCAGCTTCATGTGTAACTGGGATGTGTGACCT 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 242 GTCCGCAAAACATTTCTCTCCCGCAGCTTCATGTGTAACTGGGATGTGTGACCT 301
OY 184 GGGCACTGTGATGCTCCCTCAGTCTGCAAAATTCAGCTTGCAGACTTGCAGTAAGC 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 GGGCACTGTGATGCTCCCTCAGTCTGCAAAATTCAGCTTGCAGACTTGCAGTAAGC 361
OY 244 CTGAGAACATTTCTGTGTCTACTACTATAGAAATTTAACTGCAGCTTGGAGTCCAG 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 362 CTGAGAACATTTCTGTGTCTACTACTATAGAAATTTAACTGCAGCTTGGAGTCCAG 421
OY 304 GAAAGGAAACAGTTATACCCAGTACAGTTCAGAGTTCAGAGTTCAGAGTTCAG 363
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DB 422 GAAAGGAAACAGTTATACCCAGTACAGTTCAGAGTTCAGAGTTCAGAGTTCAG 481
OY 364 ATGATTAATTTGACAAACATAGTTCTACAGTGAATTCGTCGTCCTTTTCC 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 482 ATGATTAATTTGACAAACATAGTTCTACAGTGAATTCGTCGTCCTTTTCC 541
OY 424 TTCCAGATTAAGATCCAGATATATATACATTTGAGTGGAGTGAATGGAGATG 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 TTCCAGATTAAGATCCAGATATATATACATTTGAGTGGAGTGAATGGAGATG 601
OY 484 GTGTAATTAATTCATATGACATACAGTTCAGAGTTCAGAGTTCAGAGTTCAG 543
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DB 602 GTGTAATTAATTCATATGACATACAGTTCAGAGTTCAGAGTTCAGAGTTCAG 661
OY 544 CTAGATTTTCCGCTGTAACACAGTTTGGCATCAAAAGATTCGTAATTTGATGGA 603
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DB 662 CTAGATTTTCCGCTGTAACACAGTTTGGCATCAAAAGATTCGTAATTTGATGGA 721
OY 604 TAAAGCCTGAGTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGAGAC 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 722 TAAAGCCTGAGTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGAGAC 781
OY 664 TCAACAGTACAGCTGATGGAATGCACTTCGCTAAGAACCTGATGATTAACCAAA 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 782 TCAACAGTACAGCTGATGGAATGCACTTCGCTAAGAACCTGATGATTAACCAAA 841
OY 724 CGTCAACCTCAGGGGGCTGACGCTTTTACAGAAATGATGATGCTGCGATGTGGG 783
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DB 842 CGTCAACCTCAGGGGGCTGACGCTTTTACAGAAATGATGATGCTGCGATGTGGG 901
OY 784 TCAAGGAGTCAAAAGTTCTGAGTACAGTGAAGCAAGAAATGAGATGACTAGAGAG 843
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DB 902 TCAAGGAGTCAAAAGTTCTGAGTACAGTGAAGCAAGAAATGAGATGACTAGAGAG 961
OY 844 AAGTCCATGTGGCTGGAAGTGTGAGAGTCTGGAACAGCTGAGGCGGATGGAAGAA 903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 962 AAGTCCATGTGGCTGGAAGTGTGAGAGTCTGGAACAGCTGAGGCGGATGGAAGAA 1021
OY 904 GGCAGTGTGGGTTTATGGAAGCAAGAGAGAGGCGGCTGCTGAGAGAAACACTTG 963
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1022 GGCAGTGTGGGTTTATGGAAGCAAGAGAGAGGCGGCTGCTGAGAGAAACACTTG 1081
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OY 964 GCTACACATATGCTACTATCCAGAAAGCAACACTTAACCTCAGAGAAACATGAACACTA 1023
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DB 1082 GCTACACATATGCTACTATCCAGAAAGCAACACTTAACCTCAGAGAAACATGAACACTA 1141
OY 1024 CTAAACAGCAGCTTGAACTGATCTGGAGGCGAGAGCTTTTGGGTCTATGATTTCTT 1083
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1142 CTAAACAGCAGCTTGAACTGATCTGGAGGCGAGAGCTTTTGGGTCTATGATTTCTT 1201
OY 1084 ATATTTCTTTGGGAAGTCTCAGTGGCCACCCTGAGATTCAGACTTTTCAAGAAAT 1143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1202 ATATTTCTTTGGGAAGTCTCAGTGGCCACCCTGAGATTCAGACTTTTCAAGAAAT 1261
OY 1144 CATTTCACTGATGAGTTCATGACGAGCTCGTTGCTGAGAGACAGCTAGTGGAGAT 1203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1262 CATTTCACTGATGAGTTCATGACGAGCTCGTTGCTGAGAGACAGCTAGTGGAGAT 1321
OY 1204 GGCAGAGCTGCTCTAGACGCTGAACACTTGGATGATTAATGTTTCCGATGTGACT 1263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1322 GGCAGAGCTGCTCTAGACGCTGAACACTTGGATGATTAATGTTTCCGATGTGACT 1381
OY 1264 CAGAGCCCAACCCCTTTCTGGGAATCTGTCTCAGAGCCAGCAACTGGACATCCAGC 1323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1382 CAGAGCCCAACCCCTTTCTGGGAATCTGTCTCAGAGCCAGCAACTGGACATCCAGC 1441
OY 1324 AAGATTAATTTAAACCTTTCTGTGCTATACATCTCTGTATCCAAATGTTGATGACA 1383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1442 AAGATTAATTTAAACCTTTCTGTGCTATACATCTCTGTATCCAAATGTTGATGACA 1501
OY 1384 AAGTTGGGAGCATATTTCCATCCAGGCTTATGCCAAAGAGGCTTCCATCAGAGCTC 1443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1502 AAGTTGGGAGCATATTTCCATCCAGGCTTATGCCAAAGAGGCTTCCATCAGAGCTC 1561
OY 1444 CTGAGACCAAGTGGAGAACATTTGGCGTGAAGAGCTGACATGCAATGGAAGATTC 1503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1562 CTGAGACCAAGTGGAGAACATTTGGCGTGAAGAGCTGACATGCAATGGAAGATTC 1621
OY 1504 CCAAGAGTGAAGAAAGGATTCATCTGCAACTACACCATCTTTTACCAAGCTGAAGCTG 1563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1622 CCAAGAGTGAAGAAAGGATTCATCTGCAACTACACCATCTTTTACCAAGCTGAAGCTG 1681
OY 1564 GAAAGGATTTCTCAACAGACAGTCAAT 1589
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DB 1682 GAAAGGATTTCTCAACAGACAGTCAAT 1707
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RESULT 12
US-10-230-338-91
Sequence 91, Application US/10230338
Publication NO. US20030044934A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C92
CURRENT APPLICATION NUMBER: US/10/230,338
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17

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: PRIOR APPLICATION NUMBER: 60/063549
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: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 91
: LENGTH: 2445
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 2424
: OTHER INFORMATION: unknown base
US-10-230-338-91

Query Match      65.3%: Score 1568.4; DB 14; Length 2445;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY      4  ACGAGTGTGTGTGACATGAAAATTTGAGACAGGAGGAGAGTGTACAGCTTGTTCAC 63
Db      122 AAGACATGTGTGTGACATGAAAATTTGAGACAGGAGGAGAGTGTACAGCTTGTTCAC 181

OY      64  CTGAGCTGGGAATGTGATAGGCACTCAAGTTTTCACAGGCGATGTGTCTGAAT 123
Db      182 CTGAGCTGGGAATGTGATAGGCACTCAAGTTTTCACAGGCGATGTGTCTGAAT 241

OY      124 GTCGCGAAACATTTCTCTCCCGACCTTCATGTGTAACCTGGGATGTGAGACT 183
Db      242 GTCGCGAAACATTTCTCTCCCGACCTTCATGTGTAACCTGGGATGTGAGACT 301

OY      184 GGGCACTGTGATGCTCCCTCACTCTGCAATTCAGCTTGAGCTCTGCCACTAAGC 243
Db      302 GGGCACTGTGATGCTCCCTCACTCTGCAATTCAGCTTGAGCTCTGCCACTAAGC 361

OY      244 CTGGAACATTTCTGTGTCTACTACTACTATAGGAAAAATTTAACTGCACTTGAGCTCAG 303
Db      362 CTGGAACATTTCTGTGTCTACTACTACTATAGGAAAAATTTAACTGCACTTGAGCTCAG 421

OY      304 GAAAGGAACCAAGTTATACCAAGTACAGTTAAGAACTTACGCTTTTGGAGAAAC 363
Db      422 GAAAGGAACCAAGTTATACCAAGTACAGTTAAGAACTTACGCTTTTGGAGAAAC 481

OY      364 ATGATTAATTTGACAAACATAGTTCTACAGTGAATGCTGTCTCTTTTTC 423
Db      482 ATGATTAATTTGACAAACATAGTTCTACAGTGAATGCTGTCTCTTTTTC 541

OY      424 TTCCAAAGTAAGACCCAGATATATATACCATTTGAGTGAAGCTGAAATGGAATG 483
Db      542 TTCCAAAGTAAGACCCAGATATATATACCATTTGAGTGAAGCTGAAATGGAATG 601

OY      484 GTGTAATTAATCATATGACATCTAGAGATTAGAGACATAGCAAACTGAACAC 543
Db      602 GTGTAATTAATCATATGACATCTAGAGATTAGAGACATAGCAAACTGAACAC 661

OY      544 CTAAGATTTTCCGTGTGAAAACAGTTTGGGCATCAAAAGATGTAATGATGA 603
Db      662 CTAAGATTTTCCGTGTGAAAACAGTTTGGGCATCAAAAGATGTAATGATGA 721

OY      604 TAAAGCTGAGTTGGGCGCTGTTCATCTGATTTAAATACACCTTCGATTCAGGACG 663
Db      722 TAAAGCTGAGTTGGGCGCTGTTCATCTGATTTAAATACACCTTCGATTCAGGACG 781
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OY      664  TCAACAGTACAGCTGATGGAAGTCAACTTCGTTAAGAACCGTAAGATAAAAACCAA 723
Db      782  TCAACAGTACAGCTGATGGAAGTCAACTTCGTTAAGAACCGTAAGATAAAAACCAA 841

OY      724  CGTACAACTCAGCGGGCTCAGGCTTTTACAGAAATGTGATAGCTCTCGATGTGCGG 783
Db      842  CGTACAACTCAGCGGGCTCAGGCTTTTACAGAAATGTGATAGCTCTCGATGTGCGG 901

OY      784  TCAAGAGCTAAAGTTGTGAGTACTGAGACCCAAAGAAAAATGGAAATGACAGAGAG 843
Db      902  TCAAGAGCTAAAGTTGTGAGTACTGAGACCCAAAGAAAAATGGAAATGACAGAGAG 961

OY      844  AAGCTTCATGTGGCGCTGGAAGTGTGAGAGTCCGGAAGCAACAGCTGAGCGGATGGAAG 903
Db      962  AAGCTTCATGTGGCGCTGGAAGTGTGAGAGTCCGGAAGCAACAGCTGAGCGGATGGAAG 1021

OY      904  GGCCAGTGGGTTGTTATGGAAGAAGGCAAGAGAGCCGAGTCTAGAGAAAAACCTTG 963
Db      1022  GGCCAGTGGGTTGTTATGGAAGAAGGCAAGAGAGCCGAGTCTAGAGAAAAACCTTG 1081

OY      964  GCTACACATATGTGTACTATCCAGAAAGCAACATACTCAGAGAAACATGACCTA 1023
Db      1082  GCTACACATATGTGTACTATCCAGAAAGCAACATACTCAGAGAAACATGACCTA 1141

OY      1024  CTAACAGAGAGCTTGAAGTGCATCTGGGAGCGGAGAGCTTTGGGTCTATGATTTCTT 1083
Db      1142  CTAACAGAGAGCTTGAAGTGCATCTGGGAGCGGAGAGCTTTGGGTCTATGATTTCTT 1201

OY      1084  ATAAATCTTGTGGGAAGTCTCAGTGGCCACCCCTGAGAGATTCAGACTTTCAGAAAAAT 1143
Db      1202  ATAAATCTTGTGGGAAGTCTCAGTGGCCACCCCTGAGAGATTCAGACTTTCAGAAAAAT 1261

OY      1144  CATTTCAGTGTGATGAGTCAATGAGGCTGCGTTGCTGAGAGACAGCTAGTGTGAAT 1203
Db      1262  CATTTCAGTGTGATGAGTCAATGAGGCTGCGTTGCTGAGAGACAGCTAGTGTGAAT 1321

OY      1204  GGCAGAGCTGCTGTGAGCTGCAACACTTGGATGATGTAATGGTTCCGATGTGAGCT 1263
Db      1322  GGCAGAGCTGCTGTGAGCTGCAACACTTGGATGATGTAATGGTTCCGATGTGAGCT 1381

OY      1264  CAGAGCCACACCCCTTCTGAGGAATCTGTCTCAGGCGCAGCACTGAGCAATCCAGC 1323
Db      1382  CAGAGCCACACCCCTTCTGAGGAATCTGTCTCAGGCGCAGCACTGAGCAATCCAGC 1441

OY      1324  AAGATTAATTTAAACCTTTCTGCTGTATATACATCTCTGTGTATCCAAATGTTGATACA 1383
Db      1442  AAGATTAATTTAAACCTTTCTGCTGTATATACATCTCTGTGTATCCAAATGTTGATACA 1501

OY      1384  AAGTTGGCGAGCCATATTCATCCAGGCTTATGCAAGAAAGGCGTTCATCAGAAAGTC 1443
Db      1502  AAGTTGGCGAGCCATATTCATCCAGGCTTATGCAAGAAAGGCGTTCATCAGAAAGTC 1561

OY      1444  CTGAGACCAAGGTGAGAACATTTGGCGTGAAGAGCGTACAGATCAATGAAAGATTC 1503
Db      1562  CTGAGACCAAGGTGAGAACATTTGGCGTGAAGAGCGTACAGATCAATGAAAGATTC 1621

OY      1504  CCAAGAGTGAAGAAAGGATATCTCTGCAACTACACATCTTTTACCAGCTGAAGCTG 1563
Db      1622  CCAAGAGTGAAGAAAGGATATCTCTGCAACTACACATCTTTTACCAGCTGAAGCTG 1681

OY      1564  GAAAGATTTCTCCAGACAGCTCAAT 1589
Db      1682  GAAAGATTTCTCCAGACAGCTCAAT 1707
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RESULT 13

US-10-218-631-91

: Sequence 91, Application US/10218631

: Publication No. US20030045687A1

: GENERAL INFORMATION:

: APPLICANT: Baker, Kevin P.

: APPLICANT: Desnoyers, Luc

OY	1144	CATTTCATGATGAGGTCAATGCAAGGCTCCGTTCTGAGACACAGCTAATGCTGAAGT	1203
Db	1262	CATTTCATGATGAGGTCAATGCAAGGCTCCGTTCTGAGACACAGCTAATGCTGAAGT	1321
OY	1204	GGCAAAAGTCTGCTCTAGACGTGAACAATTTGGATGATGAATGGTTTCCGATGTGACT	1263
Db	1322	GGCAAAAGTCTGCTCTAGACGTGAACAATTTGGATGATGAATGGTTTCCGATGTGACT	1381
OY	1264	CAGAACCCACACCCCTTTCCTGGGAATCTGTGTCTCAGGCCAGCAACTGACGATCCAGC	1323
Db	1382	CAGAACCCACACCCCTTTCCTGGGAATCTGTGTCTCAGGCCAGCAACTGACGATCCAGC	1441
OY	1324	AAGATTAATTTAAACCTTTCTGGGTCATTAACATCTGTGTATTCGAATGTTGATGACA	1383
Db	1442	AAGATTAATTTAAACCTTTCTGGGTCATTAACATCTGTGTATTCGAATGTTGATGACA	1501
OY	1384	AAGTTGGCGAGCCATATTCATCCAGGCTTATGCCAAAGAAAGGCGTTCCATCAGAAAGTCC	1443
Db	1502	AAGTTGGCGAGCCATATTCATCCAGGCTTATGCCAAAGAAAGGCGTTCCATCAGAAAGTCC	1561
OY	1444	CTGAGACCAAGSTGGAGACATTTGGCGTGAAGAGGTCACCATACATGGAAAGAGATTC	1503
Db	1562	CTGAGACCAAGSTGGAGACATTTGGCGTGAAGAGGTCACCATACATGGAAAGAGATTC	1621
OY	1504	CCAAGAGTGAAGAAAGGATATTCATCTGCAACTACACCAATTTTACCACCTGAAGGTG	1563
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RESULT 15
 US-10-216-159A-91
 : Sequence 91, Application US/10216159A
 : Publication No. US20030069397A1
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Gerritsen, Mary
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Smith, Victoria
 : APPLICANT: Stephan, Jean-Philippe F.
 : APPLICANT: Watanabe, Colin L.
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P350P1C6
 : FILE REFERENCE: P350P1C6
 : CURRENT APPLICATION NUMBER: US/10/216,159A
 : CURRENT FILING DATE: 2002-08-09
 : PRIOR APPLICATION NUMBER: 10/119,480
 : PRIOR FILING DATE: 2002-04-09
 : PRIOR APPLICATION NUMBER: 60/059113
 : PRIOR FILING DATE: 1997-09-17
 : PRIOR APPLICATION NUMBER: 60/062287
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/063549
 : PRIOR FILING DATE: 1997-10-28
 : PRIOR APPLICATION NUMBER: 60/064103
 : PRIOR FILING DATE: 1997-10-31
 : PRIOR APPLICATION NUMBER: 60/0659873
 : PRIOR FILING DATE: 1997-12-17
 : PRIOR APPLICATION NUMBER: 60/078910
 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/079294
 : PRIOR FILING DATE: 1998-03-25
 : PRIOR APPLICATION NUMBER: 60/079656
 : PRIOR FILING DATE: 1998-03-26
 : PRIOR APPLICATION NUMBER: 60/079738

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; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 91
; LENGTH: 2445
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2424
; OTHER INFORMATION: unknown base
US-10-216-159A-91

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Best Local Similarity	99.3%	Pred. No. 0		
Matches 1575	Conservative	0	Mismatches 11	Indels 0
				Caps 0

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Dd	182	CTCAGCTGGGATGTGCATCAGGCAACTCAAGTTTTTTCACCAAGGATGTGTGTGAAT	241
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Dd	542	TTCCAAGATATACGATCCAGATATATTAACCATTTGAGGTGAAGCTGA AATGAGATG	601
OY	484	GTGTAATTAATTCATATGTGACATACGTGGAGATTAGAACATATGCGAAAACTGAAACAC	543
Dd	602	GTGTAATTAATTCATATGTGACATACGTGGAGATTAGAACATATGCGAAAACTGAAACAC	661
OY	544	CTAAGATTTTCCGTGTGA AACACAGTTTTTGGGCATCAAAACGATGATTTCAAAATTTGATGGA	603
Dd	662	CTAAGATTTTCCGTGTGA AACACAGTTTTTGGGCATCAAAACGATGATTTCAAAATTTGATGGA	721
OY	604	TAAAGCCTGAGATTTGGCGCCTGTTTCATCTGATTTAAATACACACTTGCATTCAGAGACG	663
Dd	722	TAAAGCCTGAGATTTGGCGCCTGTTTCATCTGATTTAAATACACACTTGCATTCAGAGACG	781
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Dd	782	TCAACAGTACAGCTGAGTGAAGTGAAGTCAACTTCGCTAAGAACCCGTAAAGGATTA AAAACCAA	841
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OY 964 GCTACACATATGTAGTACTATCCAGAAAGCAACATAACCTCAGAAAACATGAAACACTA 1023
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OY 1084 ATATTTCTCTTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGACTATTCAGAAAAAT 1143
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Db 1202 ATATTTCTCTTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGACTATTCAGAAAAAT 1261
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OY 1144 CATTTCAAGTGCATGTAGAGTCAATGCAAGGCGCTGCTGAGAGCCAGCTAGTGGTGAAGT 1203
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OY 1204 GGCAAAAGCTGTGCTCTAGACGCTGAACACTTGATGATGATGATGATGATGATGATGAT 1263
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OY 1384 AAGTTGGGAGGACCATATTCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAAAGGTC 1443
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      |||||||
Db 1562 CTGAGACCAAGGTGGAAGACATTTGGCGTGAAGAGCGGTACGATCAGATGGAAGAGATTC 1621
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OY 1504 CCAAGAGTGAAGAGGATATCATCTGCAACTACACCATCTTTACCAAGCTGAAGGTG 1563
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Db 1622 CCAAGAGTGAAGAGGATATCATCTGCAACTACACCATCTTTACCAAGCTGAAGGTG 1681
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OY 1564 GAAAAGATTTCTCCAAGACAGTCAAT 1589
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Db 1682 GAAAAGATTTCTGTAAGCAGCGCCAT 1707
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Job time : 494 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 20:13:52 ; Search time 4964 seconds
(without alignments)
11760.546 Million cell updates/sec

Title: US-09-892-949-1
Perfect score: 2402
Sequence: 1 ggcacgaggtgtgtgtgcag.....atgagacctcggagctca 2402

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	554.6	23.1	2232 11 AK030512	AK030512 Mus muscu
2	286.4	11.9	663 10 BB617934	BB617934 BB617934
3	230.6	9.6	612 29 AG138991	AG138991 Pan trogl
4	197	8.2	653 13 BU455838	BU455838 603772418

5	163.8	6.8	459 28 A0022781	A0022781 HS_2180_A
6	155.2	6.5	592 14 CA561173	CA561173 K0283D09-
7	149.4	6.2	479 14 CA560924	CA560924 K0279C07-
8	134.6	5.6	553 14 CA559889	CA559889 K0266C03-
9	133.2	5.5	546 14 CA555774	CA555774 K0202F08-
10	129	5.4	487 13 B0560019	B0560019 H4061G10-
11	129	5.4	518 14 CA561193	CA561193 K0283F09-
12	129	5.4	523 14 CA559290	CA559290 K0256G09-
13	128.6	5.4	756 28 B2147466	B2147466 CH230-406
14	126.6	5.3	924 13 B038538	B038538 AGENCOURT
15	125.6	5.2	474 28 A0815177	A0815177 HS_-3265_B
16	124	5.2	763 13 B0288431	B0288431 603607401
17	104.4	4.3	369 28 A0802743	A0802743 HS_-3222_A
18	102.8	4.3	642 14 CB512958	CB512958 ssalirp54
19	89.2	3.7	828 13 B0271003	B0271003 603508092
20	87.4	3.6	825 14 CB518939	CB518939 UT-M-GH0-
21	80.6	3.4	751 13 B0770280	B0770280 UT-M-F10-
22	80.4	3.3	704 14 CD468030	CD468030 Leuko81_8
23	77.4	3.2	625 9 AV359708	AV359708 AV359708
24	76.6	3.2	1201 13 BX382126	BX382126 BX382126
25	76	3.2	2804 11 AK089305	AK089305 Mus muscu
26	75.6	3.1	698 14 CD350375	CD350375 UT-M-PY0-
27	75.4	3.1	629 14 CD561293	CD561293 B0428B03-
28	75.4	3.1	2792 11 BC040954	BC040954 Homo sapi
29	74.8	3.1	587 12 BG921322	BG921322 602824173
30	74.4	3.1	522 4 BX528149	BX528149 R2PD Mus
31	70.6	2.9	669 13 B0322304	B0322304 603854025
32	66.6	2.8	544 14 CA884372	CA884372 B0109G07-
33	66.4	2.8	1201 13 BX359249	BX359249 BX359249
34	64	2.7	435 14 CB792919	CB792919 AMGNDC:N
35	63.8	2.7	580 14 CB606942	CB606942 AMGNDC:C
36	63	2.6	559 9 AA457864	AA457864 vF73G05_X
37	62.2	2.6	531 28 BH056800	BH056800 RPCI-24-2
38	62.2	2.6	613 28 A2257344	A2257344 RPCI-23-1
39	61.2	2.5	394 12 B1024387	B1024387 CM3-MT029
40	60.8	2.5	762 10 BG743042	BG743042 602632165
41	59.6	2.5	1098 9 AL549432	AL549432 AL549432
42	59.4	2.5	384 28 BH042598	BH042598 RPCI-24-3
43	59.4	2.5	578 14 CA885002	CA885002 B0115C02-
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ALIGNMENTS

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LOCUS AK030512
DEFINITION Mus musculus adult male pituitary gland cDNA, RIKEN full-length
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ACCESSION AK030512
VERSION AK030512.1 GI:26326508
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 2049374
PUBMED 11042159

OY	2088	GTACACGAGCCCTTCAGCCGATTTGTCGCCCGGGAAAAATTTTGGAGACCTCCAGTT	2147
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Db	920	TTAACTGAGGTGGTTCTTGAAGACCTCCACAGCAGTGTTCACAAATGGCCGAGAGCGG	979
OY	2208	CGCCACAGAGCAAGAAGACAGCTCTCTTTCTGTGTCAAAGTTTAGTACCGAGATCATCTG	2267
Db	980	TATCTCAGAAATGGCGCAGGACACCTTCGTCTTCCCTGTCTAGAGATCCAGGGCTATGCGCTCC	10399
OY	2268	TGTAGAGGAGAGGCCCCCAATCCATATTTTGAAAAATTCAGTGACAGCCAGGAAATTTCTT	2327
Db	1040	CGTGAAGACCCAAGTCCAGAAATCCATTATTGAAAAATTCAGGACACACAGGGAATTTCTT	10999
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Db	1100	GTGCATGAGAAATATCCGAGACACAGCAAGAAAGAAAGTCTAGTGCTGTCTATGGCATGA	11599
OY	2388	ACCTCGGGGCGCTCA	2402
Db	1160	GTCTCAGAAACTGA	1174

RESULT 2	
BB617934	
LOCUS	BB617934
DEFINITION	BB617934 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 5330424C19 5', mRNA sequence.

ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION
Mus musculus	Mus musculus (house mouse)	EST	BB617934.1	BB617934
Mus musculus				GI:15396442

REFERENCE
AUTHORS
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 663)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaigaki, T., Hara, A.

TITLE
 JOURNAL
 COMMENT
 Contact: Yoshihide Hayashizaki
 Unpublished
 RIKEN Mouse ESIS (Arakawa, T., et al. 2001)

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, U., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).
Yamanaka, T., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Harai, A., Itoh, M., Kawai, J., Shibata, K., Aikawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Funct. Genomics* 2 pre, 172-Lt6 (2001).
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.

FEATURES	Location/Qualifiers
source	1. .663

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BASE COUNT
ORIGIN
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/mol_type="mRNA"
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/tissue_type="pituitary gland"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="RIKEN full-length enriched, adult male
pituitary gland"
/notes="Site.1: SalI; Site.2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGGAGAGAGAGATCCACAGACTCTTTTCTTTTCTTTT 3', cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 3.0 and subtraction to Rot = 100.0. Second strand
cDNA was prepared with the primer adapter of sequence 15'
GAGGAGAGAGATTCGAGTTAATTAATATATCCCCCCCCC 3'. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

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Query Match	11.9%;	Score 286.4;	DB 10;	Length 663;
Best Local Similarity	78.2%;	Pred. No. 1.9e-73;		
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OY	1428	GTTCCATCAGAGGTCCTGAGACCAAGGTGAGAACATTGGCGTGANGAGCGTCAGATC	1487	
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OY	1488	ACATGGAAGAAGATTTCCCAAGAGTGAAGAAAGGTATCATCTCACTCACTCACCATCGTT	1547	
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 DB 629 CCTGCTTAATAATATTATACCATGGCTCCGA 662
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 DEFINITION AG138991
 ACCESSION AG138991.1 GI:16668669
 VERSION GSS.
 KEYWORDS Pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 REFERENCE 1
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Matanabe, H. and Sakaki, Y.
 TITLE BAC end sequences of library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 612)
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Matanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Tsurumi-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpesgsc.riken.go.jp, URL: http://hgp.9sc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Rad process and may have higher chance of clone tracking errors.
 PRIMERS
 Sequencing: -21M13
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
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 BASE COUNT 155 a 172 c 120 g 165 t
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 Best Local Similarity 96.1%; Pred. No. 8.4e-57;
 Matches 247; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
 QY 1886 TTCAAGATAGCTAAACCTGAAGAGCTGTGACTCTGTGACACAGACAGACAGAT 1945
 DB 332 TTTCAGATATAGCTAAACCTGAAGAGCTGTGATGAGAAA-TGACACAGAAAGACAGAT 274
 QY 1946 CTTAAACCATGTTCCACCCAGTGACAGTGGTGATTTGACAAAGTTGGTGAGTACTT 2005
 DB 273 CTTAAACCATGTTCCACCCAGTGACAGTGGTGATTTGACAAAGTTGGTGAGTACTT 214
 QY 2006 TGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAGCGGTGAGAAACAAATTT 2065
 DB 213 TGGGATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAGCGGTGAGAAACAAATTT 154
 QY 2066 AGAGGGGAAAGATGGGTATGTGACTGCCCTTTCAGGCTGATTTCCCTGGGGAA 2125
 DB 153 AGAGGGGAAAGATGGGTATGTGACTGCCCTTTCAGGCTGATTTCCCTGGGGAA 94
 QY 2126 AAGTTTGGAGAGCTCC 2142

DB 93 GAGTTTGGAGAGCTCC 77
 RESULT 4
 B0455838 653 bp mRNA linear EST 29-NOV-2002
 LOCUS 603772418F1 CSEORBN14 Gallus gallus CDNA clone Chest708c5 5', mRNA sequence.
 DEFINITION B0455838
 ACCESSION B0455838.1 GI:25945149
 VERSION EST.
 KEYWORDS Gallus gallus (chicken)
 SOURCE Gallus gallus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.M., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 2235534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 FEATURES
 source
 1..653
 location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer"
 /db_xref="taxon:9031"
 /clone="Chest708c5"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEORBN14"
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 BASE COUNT 233 a 110 c 134 g 176 t
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 Query Match 8.2% Score 197; DB 13; Length 653;
 Best Local Similarity 58.7%; Pred. No. 9.5e-47;
 Matches 360; Conservative 0; Mismatches 250; Indels 3; Gaps 1;
 QY 1281 TCCTGGGATCTGTCTCAGGCCACGACGTGACATTCGACAAAGTTGGAGCCCAAT 1340
 DB 14 TCATGGCAGTATATATCAAAATTTCTCAAGAGGAAACTAACAATAAATA 73
 QY 1341 TCTGAGCTTAACATCTGTGATATCCATGTTGACGACAAAGTTGGAGCCCAAT 1400
 DB 74 TTGTATGCTCAACATGTCATGATTCCTATCTATGAAATTAAGTGACAGCTCAAT 133
 QY 1401 TCATCCAGGCTTATGCCAAGAGGCGTTCATCAGAGGTCTCGAAGCAAGGTGGAG 1460

Db 134 TCCATCAACAACTATATGTCAGAAAAAGACCATCAAGAGCCCTGTGGCTGATACGGGT 193
QY 1461 AACATTGGCGGTGAAGAGCGTCAGATCAGATGGAAGAGATTCGCCAAGATGAGAGAA 1520
Db 194 TTTCCAGGCAAAATAGATTACAAATTAATGAATGCAATTTCAAGATTAAGATTAAGAT 253
QY 1521 GGTATCATCTGCACATACACATCTTTTACCAAGCTGAAGGTGAAGAGATTCCTCAAG 1580
Db 254 GGGTTATTAGTAGTACATACATATTTTATAAACCTGAAGGTGGAAGAGATGAATGA 313
QY 1581 ACAGTCAATTCAGCATCTTTGACAGTGGCTGAGTCCCTGGAAGCAAGACCTCTTAC 1640
Db 314 ACAGTCAACTGATGTGTGACAGTACAGTACAGTCAAGTCTTACAGGCTAATACACATAC 373
QY 1641 ATTGTTCAGTCAATGTCAGACACACACATGCTGGGGGAACCAAGGACACATATATTC 1700
Db 374 ACTGTCTATATCTATGAGCAACAGAGCTGTGGAACCAAGTGAAGCCAAACATTC 433
QY 1701 AAGACATTTGTCATTCAGTGTCTTGAAGATATCTCTCATATCTCTGATTTGGAGAGC 1760
Db 434 AACATTTGAAATTCATATAAGAACGTTATTTTCAATTCATACACAGTTGGATTACG 493
QY 1761 CTTCCTATCTCTCATATATCTGACAGTGGCATATGCTCAAAAACCAACCAATTTGACT 1820
Db 494 ATGTGTTCTCTGTTAGGCTTTGGATTAACGTGCATTAATGAAGAAAC--ACGTGTTTAA 550
QY 1821 CATCTGTGTGGCCACCGCTCCCAACCCCTGCGAAGATGATATGACCATATGCGATGA 1880
Db 551 AAGGTTTGTGGCGCTGATGATACCAATCTGACAGAGCGTTGACAGTGGCGCTCTT 610
QY 1881 GATGATTTCAAG 1893
Db 611 GATGATCTATG 623

RESULT 5
LOCUS A0022781 459 bp DNA linear GSS 16-JUN-1998
DEFINITION HS_2180_A2_B11_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone plate-2180 Col-22 Row-C, genomic survey
sequence.
ACCESSION A0022781 GI:3220989
VERSION A0022781
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2180 row: C column: 22
Class: BAC ends
High quality sequence stop: 459.
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/organism="Homo sapiens"
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/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
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BASE COUNT 132 a 81 c 113 g 130 t 3 others
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Best Local Similarity 98.2%; Pred. No. 6e-37;
Matches 165; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 208 TAGATGGAAGTCAACTGCTAGAGAACCGTAAAGATTAACCAAGCTACACCTACG 267
QY 738 GGGCTGCAGCCTTTTACAGATATGTCATAGCTCTGCGATGCGGTCAAGAGTCAAG 797
Db 268 GGGCTGCAGCCTTTTACAGATATGTCATAGCTCTGCGATGCGGTCAAGAGTCAAG 327
QY 798 TTCTGAGTACTGAGCCCAAGAAAAATGGATGACTGAGAGAA 845
Db 328 TTCTGAGTACTGAGCCCAAGAAAAATGGATGACTGAGAGAA 375
RESULT 6
LOCUS CA561173 592 bp mRNA linear EST 19-NOV-2002
DEFINITION K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
ACCESSION CA561173
VERSION CA561173
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Staag,C.A.,
Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
TITLE Systematic Analyses of NIA Mouse Fertilized Egg cDNA Library
(Long)
JOURNAL Unpublished
COMMENT Other-ESTs: K0283D09-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nigmsun.grc.nia.nih.gov
Plate: K0283 row: D column: 09
Seq primer: M13 Reverse
High quality sequence stop: 592
POLYA-No.
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source location/Qualifiers
1..592
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/clone="NIA:K0283D09 IMAGE:30052652"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_11b="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site.1: SalI; Site.2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://nigmsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). (PMID: 11544191)). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.

Db	Accession	Version	Keywords	Source	Organism	Title	Journal	Comment
508	ACTGAGATTGACACATAG	528						
459	ATTGCATTATATCTCCATAG	479						
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CA559989								
LOCUS								
DEFINITION	CA559989	553 bp	mrna	linear	EST 19-NOV-2002			
ACCESSION	K0266C03-5N	NIA Mouse Unfertilized Egg cDNA Library (Long)	Mus					
VERSION	CA559989	musculus cDNA clone NIA:K0266C03 IMAGE:30051002 5'	mrna sequence.					
KEYWORDS	CA559989.1	GI:25104613						
SOURCE	EST.							
ORGANISM	Mus musculus (house mouse)							
	Mus musculus							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
REFERENCE	1 (bases 1 to 553)							
AUTHORS	Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A.,							
	Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.							
	Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library							
	(Long)							
	Unpublished							
	Other_ESTs: K0266C03-3							
	Contact: Dawood B. Dudekula							
	Laboratory of Genetics							
	National Institute on Aging/National Institutes of Health							
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA							
	Email: cdna@gsun-grc.nia.nih.gov							
	Plate: K0266	row: C	column: 03					
	Seq primer: M13 Reverse							
	High quality sequence stop: 553							
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/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_1ib="NTA Mouse Unfertilized Egg cDNA Library (long
) "
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NTA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 148 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen):
5'-GACAGCTTACATGATCGGAGCGGCCGCTTTTCTTTTCTTTT-3'},
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker IL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-5. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NTA)."
BASE COUNT
144 a 136 c 114 g 159 t
ORIGIN
Query Match 5.6%; Score 134.6; DB 14; Length 553;
Best Local Similarity 64.2%; Pred.NO. 3.6e-28;

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Matches	228:	Conservative	0:	Mismatches	109:	Indels	18:	Gaps	1:
QY	131	AAACATTCCTCTCTCCAGCCTTCAGTGTTAACTGGGGATGATGTGAGCTGGGCACT	190						
Db	213	AAACCTTCATGAATTAACGAGCCTCTGGGGGTGAGACGCTGGAAATTAATGTGAGACTTGGCACC	272						
QY	191	GTGATGCTCCCTCAGCTCTGCAAAATTCAGCCTTGGCAGCTTGGCAGCTTAAGCTTGACA	250						
Db	273	GTGGGCAATTCCTCTCCCTCTGCAAAATTCAGCCTTGGCAGCTTGGCAGCTTAAGCTTGACA	332						
QY	251	CATTTCCTGCTGACTACTATAGAGAAAATTTAACTGAGCCTTGGAGTCCGAGGAAAGA	310						
Db	333	CATTTCCTGAGCTCTTTTACTCTTGACAGAAATCTAATCTTGAGAGACCAAGAAAGA	392						
QY	311	AACAGTTATACCCAGTACAGACTTAAAGAGAACTTACGCTTTTGAGAGAAAACATGATAA	370						
Db	393	AACCAATATATACAGCTACATTTGAGACTTGTACTTACCTCCATAGA	438						
QY	371	TTGTACAAACAATAGTTCTACAGTGAATAATCGTGCTTGCTCTTTTTCCTCCAG	430						
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QY	431	AATAAGATCCCAAGTAAATTAATACACTGAGAGTGAAGCTGAATAATGAGATGTGT	485						
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LOCUS	CA555774	546 bp	mRNA	linear	EST 19-NOV-2002				
DEFINITION	K0202F08-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus								
ACCESSION	musculus cDNA clone NIA:K0202F08 IMAGE:30044899 5', mRNA sequence.								
VERSION	CA555774								
KEYWORDS	CA555774.1 GI:25100137								
SOURCE	EST.								
ORGANISM	Mus musculus (house mouse)								
REFERENCE	Mus musculus								
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 546)								
TITLE	Piao Y., Karauli G.J., Dudekula D.B., Qian Y., Luo A., Steag, C.A., Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H. Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (Long)								
JOURNAL	Unpublished								
COMMENT	Other ESTs: K0202F08-3 Contact: Dawood B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@igsun.grc.nia.nih.gov Plate: K0202 row: F column: 08 Seq primer: M13 Reverse High quality sequence stop: 546 POLYA=No.								
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	/strain="C57BL/6J"								
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	/clone="NIA:K0202F08 IMAGE:30044899"								
	/tissue_type="Unfertilized Egg"								
	/lab_host="DH10B"								
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	/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were								

[illegible]

extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen):
5'-P₆ACTAGTTCCTAGATCGGAGCGGCGCCCTTTTCTTTT-3',
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
lone-linker LR-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA).

BASE COUNT 140 a 137 c 112 g 157 t

ORIGIN

Query Match 5.5%; Score 133.2; DB 14; Length 546;
Best Local Similarity 64.2%; Pred. No. 9.4e-28;
Matches 226; Conservative 0; Mismatches 108; Indels 18; Gaps 1;

QY 131 AACATTCTCTCTCCACGCTTCATGTGTTAACTGGGGATGATGAGCTGGCACT 190
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Db 213 AACCTTCATGATGAATACAGCCTCTGGGTGACCACTGATGAATATGAGCTTGGCACT 272
191 GTGATGTCCTCCCTCCTCCTGCAATTCAGCTGTCAGCTGCGCAGCTGAAGCTGAGAA 250
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Db 273 GTGGGCATTCCTCTCTCTCTGCAATTCAGCTGTCAGCTGCGCAGCTGAAGCTGAGAA 332
251 CATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGAGTCCAGAAAGA 310
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Db 333 CATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGAGTCCAGAAAGA 392
311 AACCGTATATACCCAGCTACAGAGTAAAGAACTTACCTTTGGAGAAAAACATGATAA 370
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Db 333 AACCATATATACCCAGCTACAGAGTAAAGAACTTACCTTTGGAGAAAAACATGATAA 438
371 TTGTACAAACATAGTCTTACAGAGTAAAGAACTTACCTTTGGAGAAAAACATGATAA 430
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Db 439 ----AAAGCAATTTAGTGAACATGCTACAGAGCTTCATATTTTCCCGTCTCG 494
431 AATAACGATCCAGATTAATTTATACCTTGGAGTGAAGCTGAAAAATGAGAT 482
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Db 495 TGCATATGCCCGACAGACATGTGAGTGAAGTGAACGCTCAAAATGAGAT 546

RESULT 10
B0560019 487 bp mRNA linear EST 20-JUN-2002
LOCUS H4061G10-5 NIA Mouse 7.4K cDNA Clone set Mus musculus cDNA clone
DEFINITION H4061G10 5', mRNA sequence.
ACCESSION B0560019
VERSION B0560019.1 GI:21460904
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 487)
REFERENCE Vanburen V., Piao Y., Dudekula D.B., Qian Y., Carter M.G., Martin
P.R., Stagg C.A., Bassey U., Alba K., Hamantani T., Kargul G.J.,
Luo A.G., Kelsio J., Hilde W., and Ko M.S.H.
Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
TITLE Genome Res. 12 (12), 1999-2003 (2002)
JOURNAL MEDLINE 22354164
PUBMED 12466305
COMMENT Other ESTs: H4061G10-3
Contact: Yong Qian
Laboratory of Genetics

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cda@nigmsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://ligsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
Plate: H4061 row: G column: 10
Seq primer: -21M3 Reverse
High quality sequence stop: 487
POLYA-No.

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/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

BASE COUNT 123 a 123 c 98 g 143 t

ORIGIN

Query Match 5.4%; Score 129; DB 13; Length 487;
Best Local Similarity 71.0%; Pred. No. 1.5e-26;
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 131 AACATTCTCTCTCCACGCTTCATGTGTTAACTGGGGATGATGAGCTGGCACT 190
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Db 213 AACCTTCATGATGAATACAGCCTCTGGGTGACCACTGATGAATATGAGCTTGGCACT 272
191 GTGATGTCCTCCCTCCTCCTGCAATTCAGCTGTCAGCTGCGCAGCTGAAGCTGAGAA 250
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Db 273 GTGGGCATTCCTCTCTCTCTGCAATTCAGCTGTCAGCTGCGCAGCTGAAGCTGAGAA 332
251 CATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGAGTCCAGAAAGA 310
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Db 333 CATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGAGTCCAGAAAGA 392
311 AACCGTATATACCCAGCTACAGAGTAAAGAACTTACCTTTGGAGAAAAACATGATAA 370
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371 T 371
QY 453 T 453
Db 453 T 453

RESULT 11
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LOCUS K0283F09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
DEFINITION K0283F09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
ACCESSION CA561193
VERSION CA561193
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 518)
REFERENCE Piao Y., Kargul G.J., Dudekula D.B., Qian Y., Luo A., Stagg C.A.,
Martin P., Alba K., Tanaka T., and Ko M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)
TITLE Unpublished
JOURNAL Other ESTs: K0283F09-3
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0283 row: F column: 09
Seq primer: M13 Reverse
High quality sequence stop: 518
POLYA-No.

FEATURES
source

Location/Qualifiers
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/clone="NIA:K0283F09 IMAGE:30052676"
/tissue_type="unfertilized Egg"
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/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project for the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGCGACGCCGCCCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 129 a 134 c 105 g 150 t
ORIGIN

Query Match 5.4% Score 129; DB 14; Length 518;
Best Local Similarity 71.0%; Pred. No. 1.6e-26;

Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

OY 131 AAACATTCTCTCCCGACGCTTCATGTTAACTGGGATGATGAGACCTGGGACT 190
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Db 213 AAACCTCATGAATAAAGAGCTCTGGGTGTCAAGCGTGAATATGTGGACCTTGGCACT 272
OY 191 GTGGATGCTCCCTCACTGTGCAAAATTCAGCTGGAGCTGTGCCAGCTAAGCTGAGAA 250
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Db 273 GTGGGCAATCTCTCTCTCTGCAAAATTCAGCTGGAGCTGTGCCAGCTAAGCTGAGAA 332
OY 251 CATTTCTGTGTCTACTACTATAGGAAAAATTTAACTGCTGAGTGGAGTCCAGAGAA 310
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Db 333 CATTTCTGTGTCTCTCTCTGCAAAATTCAGCTGGAGCTGTGCCAGCTAAGCTGAGAA 392
OY 311 AACCAGTTATACCCAGTACAGAGATTAAAGAACTTACGCTTTGGAGAAAAACATGATTA 370
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Db 393 AACCAGTTATACCCAGTACAGATTTGACTTTGACTTACTCTATGAGAAAAACATTTATAG 452
OY 371 T 371
Db 453 T 453

RESULT 12
CA559290 523 bp mRNA linear EST 19-NOV-2002
LOCUS

DEFINITION K0256G09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
musculus cDNA clone NIA:K0256G09 IMAGE:30050096 5', mRNA sequence.
ACCESSION CA559290
VERSION 1
KEYWORDS GI:25103871
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murine; Mus.
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
Mus musculus

REFERENCE

1 (bases 1 to 523)
Piao, Y., Kargul, G.D., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A.,
Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)

JOURNAL

CONTACT: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0256 row: G column: 09
Seq primer: M13 Reverse
High quality sequence stop: 523
POLYA-No.

FEATURES
source

Location/Qualifiers
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/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project for the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGCGACGCCGCCCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 129 a 134 c 107 g 153 t
ORIGIN

Query Match 5.4% Score 129; DB 14; Length 523;
Best Local Similarity 71.0%; Pred. No. 1.6e-26;

Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

OY 131 AAACATTCTCTCCCGACGCTTCATGTTAACTGGGATGATGAGACCTGGGACT 190
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Db 213 AAACCTCATGAATAAAGAGCTCTGGGTGTCAAGCGTGAATATGTGGACCTTGGCACT 272
OY 191 GTGGATGCTCCCTCACTGTGCAAAATTCAGCTGGAGCTGTGCCAGCTAAGCTGAGAA 250
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OY		311	AACCA GTTATACCCAGTACACAGCTTAAGACAACCTTAGCCTTTGGAGAAAAAACATGATAA	370
Db		393	AACCAATGATACCAAGCTACATTTGACCTTTGACTTACCTCATGSAAAAACATTTATAG	452
OY		371	T 371	
Db		453	T 453	
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BZ147466/c				
LOCUS	BZ147466	756 bp	DNA	linear GSS 11-OCT-2002
DEFINITION	CH230-406E16.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone			
ACCESSION	CH230-406E16			Rattus norvegicus genomic clone
VERSION	BZ147466			
KEYWORDS	BZ147466..1 GI:23788403			
SOURCE	GSS.			
ORGANISM	Rattus norvegicus (Norway rat)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
REFERENCE	1 (bases 1 to 756)			
AUTHORS	Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,			
	A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de			
	Jong,P. and Fraser,C.M.			
TITLE	Rat BAC End Sequences from Library CHORI-230 MboI segment			
JOURNAL	Unpublished			
COMMENT	Other_GSSs: CH230-406E16..TV			

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CHORI-230 Rat (BN/SSNhd/MCM) BAC library produced by
Pleter de Jong"
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BASE COUNT
  205 a 164 c 185 g 202 t
ORIGIN
  Query Match 5.4%; Score 128.6; DB 28; Length 756;
  Best Local Similarity 77.9%; Pred. NO. 2.8e-26;
  Matches 155; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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[illegible]

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OY	1045	ATCGGGAGGGGAAGCTTTGGSGTGCTATGATTTCCTATATTCCTTGGGAAGTCG	1104
Dd	79	TTCGTGGTGGGCCAACACGCACGTGTGTGTGACTCTTTTAACCTCTTGGCAAGTCCC	20
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Dd	19	AAGAGGCCATCACTGAGGAT	1

RESULT	14
LOCUS	BQ938538
DEFINITION	BQ938538 924 bp mRNA linear EST 21-AUG-2002
ACCESSION	AGNCNCOURT_8931844 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466061
VERSION	5'', mRNA sequence.
KEYWORDS	BQ938538 BQ938538.1 GI:22354016
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	1 (bases 1 to 924)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) unpublished Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: The Cepko Laboratory, CNSA Library Preparation: Life Technologies, Inc.

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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1989 Row: m Column: 06
High quality sequence stop: 636.
Location/Qualifiers
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Nc1;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

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	Query Match	5.38;	Score 126.6;	DB 13;	Length 924;
	Best Local Similarity	72.0%;	Pred. No. 1.3e-25;		
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Db	655 GTAAAGACTCAAAATGTGAAGGAGACTGGAAACTCTGGCGACACAGAAGACGCTGGCTCTAAA	714			
QY	1952 ACCATGTTCCACCCCCCAGTCAGCATGGTGATTGACAAGTTGGTGGTGAACCTTTGGCAA	2011			
Db	715 ACCATGTGCCGTCCGCCGCCGATC-----TCATTTGACAACCTGGTACTGTAACCTTTGGAAA	768			
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2003, 11:08:21 ; Search time 19 Seconds
(without alignments)
1630.081 Million cell updates/sec

Title: US-09-892-949-2

Perfect score: 3908
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678.5	17.4	708	1 US-07-797-556-2	Sequence 2, Appli
2	678.5	17.4	708	1 US-08-308-881-2	Sequence 2, Appli
3	678.5	17.4	708	2 US-09-058-263-2	Sequence 2, Appli
4	678.5	17.4	708	2 US-09-059-099-2	Sequence 2, Appli
5	678.5	17.4	708	3 US-09-058-264-2	Sequence 2, Appli
6	678.5	17.4	708	4 US-09-455-962-2	Sequence 2, Appli
7	678.5	17.4	708	5 PCT-US95-06530-2	Sequence 2, Appli
8	677.5	17.3	918	4 US-08-825-558-6	Sequence 6, Appli
9	677.5	17.3	918	4 US-09-312-611-6	Sequence 6, Appli
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11	629	16.0	572	2 US-08-419-652-5	Sequence 5, Appli
12	619	15.8	859	4 US-09-313-942-7	Sequence 7, Appli
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15	616	15.8	1158	4 US-09-313-942-26	Sequence 24, Appli
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17	517.5	13.2	836	1 US-07-923-976-4	Sequence 4, Appli
18	513.5	13.1	783	6 5422248-2	Patent No. 5422248
19	508	13.0	602	2 US-08-419-652-6	Sequence 6, Appli
20	506	12.9	863	1 US-07-923-976-8	Sequence 8, Appli
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33	404.5	10.4	1001	1 US-07-797-556-6	Sequence 6, Appli
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39	383	9.8	862	2 US-08-914-520-2	Sequence 2, Appli
40	375	9.6	979	1 US-08-308-881-6	Sequence 6, Appli
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42	375	9.6	979	2 US-09-059-099-6	Sequence 6, Appli
43	375	9.6	979	3 US-09-058-264-6	Sequence 6, Appli
44	375	9.6	979	4 US-09-455-962-6	Sequence 6, Appli
45	375	9.6	979	5 PCT-US95-06530-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-07-797-556-2
: Sequence 2, Application US/07797556
: Patent No. 5262522
: GENERAL INFORMATION:
: APPLICANT: Gearling, David P.
: TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
: NUMBER OF INVENTIONS: Inhibitory Factor
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESS: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/797,556
: FILING DATE: 19911122
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Seese, Kathryn A.
: REGISTRATION NUMBER: 32,172
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: TELEFAX: 206-587-0606
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 708 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-797-556-2

Query Match 17.4%, Score 678.5; DB 1; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e+54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKPENISCVYVYKRLNCTWSPGKETSY-QGYTVK--RTYARGE--KHD--NCTN 71
DB 126 PEKPNLSCTIVNEGKKMKCEWDGGEETHLETFNFKSWATHKTRADCKAKDPTSCVD 185
QY 72 SSTSENKASCSFFLPRTIPDNYTIEVANGDVKIS-HMTYVRLNIAKTEPPKIFRV 130
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DB 349 LVMKTLPPFEANGKILDEYVLTTRKSHLQNTYVNA--KLTVNLTDRIYATLTVRNLV 406
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QY 369 TLSWESVSQATNMTIQODKLKPFWCYNISYVPMHLKVGEPYSIOAVAKGVSEGPETK 428
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RESULT 2

US-08-308-881-2
Sequence 2, Application US/08308881

Patent No. 5783672

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

3

LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match 17.4%, Score 678.5; DB 1; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

22 PAKEDNISCVYYRKNLTCTWSPGKETSY-TQYTVK---RTYAGE---KHD---NCTTN 71
DB 126 PEKPKNLSICAIENCKKRCMEWDGGRHTLETNFTLKSEMAHFKPADKAKRDPPTSCVD 185
QY 72 SSTSEGNRASCFFELPRITIPDNYITVEAENGDCVVIS-HMTYRLENIAKTEPKIFRV 130
DB 186 YST-----VFV-----NIEVWEAENALGVTSIDHINFPVYKV-KPNPHNLV 230
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DB 231 INSELSILKLTMTNPSIKSVIT-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288
QY 191 LQPTTEVYIALRCVAVKESK-FWSDMSQKMGTEEARC-GLELMRYLKPADGRRPV 248
DB 289 LKPFTEYFRIKMKEDKGWSDMSEASGITYEDRSKAPSFMYKIDPSHTQGYRTVQ 348
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DB 527 TKKVGKNEAVLEMDQLPVQNGFIRNTITYRTIIGNETAVNDSSHTEYTLSSLSDT 586
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DB 587 LYVIRMAAYTDEGKDGPEFTTTPKPAQGEIEAIVPVCLAFLLTLLGLVFCFNKRD 646
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RESULT 3

US-09-058-263-2

Sequence 2, Application US/09058263

Patent No. 5891997

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-263-2

Query Match 17.4%; Score 678.5; DB 2; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKPENISCVYYRKNTCTSPGKETS-TOYTVK---RYAGE---KHD---NCTTN 71
DB 126 PEKPNLSICIVNEGKMKRCMDGGRHLETFNLTLSMAVHKFKADCKAKRDTPTSCYVD 185
QY 72 SSTSNNRASCSEFLPRITPNNTYEVAENGDDYIKS-HMTYMLEIAKTEPPKIRY 130
DB 186 YST-----YFV-----NIEVWEAENALGKVTSDHINFDVYV-KPNPHNLSV 230
QY 131 KPVIGIKRMIOEWIKPELAPVSSDLKYLFRFVNSTSMWEVNFARKRKDKNTYNTLG 190
DB 231 INSELSIILKLTWNPISIKSVII-LKYNIOYRTDASTWQIIP-PEDTASTRSSFTYVD 288
QY 191 LOPTEYVIALRCAYKESK-FWSMSOEMGTEEADPC-GLEIMRYLKPADAGRPRYR 248
DB 289 LKPFLEYFRIRCKMEDKGYWSDWSEASGITYEDRSKAPSEFYKIDPSHTQGYRTYQ 348
QY 249 LLMKARCAPYLEKTLGYNINWYPPESNNTLETMTNTNOQLELHGGSEFWMSMYSYL 308
DB 349 LVMKTLPPFEANGKILDEYVLLTRKSHLONTYVAT--KLTVNLTNDRIATLTVRLV 406
QY 309 GKSPVATLRIPALIOESFCIEVMQACVAEDOLVVKMOSSALDVNTWMIEMFPDVDSPT 368
DB 407 GKSDAVALTIPACDQATHPVMDLKAPEKDNMLWEMTTPRESVAKYILLEMCVLSDKAPC 466
QY 369 TLSMESVSQATNWTIOQDLKLPFCYINISVYPMLDKXGEPYSIOAVYKEGVPSEGETK 428
DB 467 ITDMOQEDGTVHRTYLRGNLAEKSCYLLITVPVYADGSGPESIKAYILKQAPSPKGPYR 526
QY 429 VENISGVATVLTWKEIPKSERGIICNTTIFYQAGSGKFSKTVYSSILQGLGELAKRT 488
DB 527 TKRVKKNNAVLEMDOLPVDVONGFIRNTTIFRTITIGETAIVNDSSTHETLSSLTSDT 586
QY 489 SYIVQMASTAGNGTNSINEKTLFSVFELLITSLIGGLLILILVYAVGLKPKNK 548
DB 587 LYMWMAVYTDGEGKDGPEFTFTTPKFAOGEEALVYVCLALLTTLGLVLCFNKNDL 646
QY 549 LTHLCMPVNPABESSIATW-----HGDDFKDL 577
DB 647 IKKHIMPVDPSPKSHIAQWSPHPTPRHNNSKDM 682

RESULT 4
US-09-059-099-2
Sequence 2, Application US/09059099
Patent No. 5925740

GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-099-2

Query Match 17.4%; Score 678.5; DB 2; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKPENISCVYYRKNTCTSPGKETS-TOYTVK---RYAGE---KHD---NCTTN 71
DB 126 PEKPNLSICIVNEGKMKRCMDGGRHLETFNLTLSMAVHKFKADCKAKRDTPTSCYVD 185
QY 72 SSTSNNRASCSEFLPRITPNNTYEVAENGDDYIKS-HMTYMLEIAKTEPPKIRY 130
DB 186 YST-----YFV-----NIEVWEAENALGKVTSDHINFDVYV-KPNPHNLSV 230
QY 131 KPVIGIKRMIOEWIKPELAPVSSDLKYLFRFVNSTSMWEVNFARKRKDKNTYNTLG 190
DB 231 INSELSIILKLTWNPISIKSVII-LKYNIOYRTDASTWQIIP-PEDTASTRSSFTYVD 288
QY 191 LOPTEYVIALRCAYKESK-FWSMSOEMGTEEADPC-GLEIMRYLKPADAGRPRYR 248
DB 289 LKPFLEYFRIRCKMEDKGYWSDWSEASGITYEDRSKAPSEFYKIDPSHTQGYRTYQ 348
QY 249 LLMKARCAPYLEKTLGYNINWYPPESNNTLETMTNTNOQLELHGGSEFWMSMYSYL 308
DB 349 LVMKTLPPFEANGKILDEYVLLTRKSHLONTYVAT--KLTVNLTNDRIATLTVRLV 406
QY 309 GKSPVATLRIPALIOESFCIEVMQACVAEDOLVVKMOSSALDVNTWMIEMFPDVDSPT 368
DB 407 GKSDAVALTIPACDQATHPVMDLKAPEKDNMLWEMTTPRESVAKYILLEMCVLSDKAPC 466
QY 369 TLSMESVSQATNWTIOQDLKLPFCYINISVYPMLDKXGEPYSIOAVYKEGVPSEGETK 428
DB 467 ITDMOQEDGTVHRTYLRGNLAEKSCYLLITVPVYADGSGPESIKAYILKQAPSPKGPYR 526

```

OY      429  VENIGKVTIITWKEIPEKSERGGIICNTIPIQADGKGCFKTYNNSITLQGLSEIKRT  488
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      527  TKVAGKNEAVLEMDQLPVQVONGFRINNTIIFRTITIGETIYVANDSSHTTEITSSLSIDT  586
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      489  SYIVQVMASTAGCTNGTINSINKTLSFSVFELIILTSLIGGLLILITVYGLKPKNK  548
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      587  LYVWMAAAYDEGGKGDGKPEFTFTTPKFAGETIATVPCVCLAFILTLGLVFCFNKRD  646
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      549  LTHLCWPTVNPNAESSIATW-----HGDEPKDL  577
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      647  IKRHWNPVDPBSKSHIAQMSPHTPPRHFNMSKDM  682
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 5
US-09-058-264-2
: Sequence 2, Application US/09058264
: Patent No. 6010886
: GENERAL INFORMATION:
: APPLICANT: Mosley, Bruce
: APPLICANT: Cosman, David J.
: TITLE OF INVENTION: Receptor for Oncostatin M
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.1
: SOFTWARE: Microsoft Word, Version 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/058,264
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/308,881
: FILING DATE: 12-SEP-1994
: APPLICATION NUMBER: US 08/249,553
: FILING DATE: 26-MAY-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Seese, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2614-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 708 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-058-264-2

Query Match      17.4%; Score 678.5; DB 3; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14

OY      22  PAKPENISCVYYRKNLCTMSPGKETSY-TQYVKK--RTYAGE--KHD--NCTTN  71
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      126  PEKPKULSCTIVGDKMKRCENMGCGEETLEINFTLKSEWATHKRAADCAKARDIPTCTVD  185
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      72  SSTSENRAASCFFLPRTIIPDNYTITVEAENGDVIRS-HNTYWRLENIKATPEPIFRY  130
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      186  YST-----VYFV-----NIEVWDAENALGKVTSDIHINFDPVYKV-KRPDPNHLV  230
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      131  KPVLGIKRNIQIEMIKPELAPVSSDLKTTLFRIVYNSISWMEVNFANRKRDKQNTNLNG  190
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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Db 231 INBELSLSLKLTWNPISKSVII-LKXNIOYRTDASTWQIP-PEDTASTSSSTFYOD 288
 QY 191 LQPFTEYIALRCAYKESK-FWSDMSQEKMGTEEEAPC-GLEIMVYLKPAEDAGRRPV 248
 Db 289 LKPFTEYVFRICOMKEDGKGYSWDSSEASGITYEDRPSKAPSFMYKIDPSHTQGYRTQ 348
 QY 249 LLEKKRKGAPVLEKTLGYNIWYPPESNTNLEETNMNTTMOQLEHLGSEFWSMISVNSL 308
 Db 349 LVKTLTPRPEDANGKILDEVTLLTRKSHLQNTVNAI-KLTIVLNTDRILATLLTVRNLY 406
 QY 309 GRSVATLIRIPAIQKESFQCIEMQACVADQLVVKMOSSALDVNTMMIMFPDVPDSEPT 368
 Db 407 GKSDAVALTIPACDPQATHPVMDLKAPEKDNMLMWEWTPRESVKKILLEMCVLSDKAPC 466
 QY 369 TLSMESVSQATNWTIOQDLKAFPCWYNISVYPM.LHDKYGEFYSTQYAKESVSEGEPTK 428
 Db 467 ITDMQEDGTVHTLYLRGNLASKCYLLITVPYVADGSGSPESIKAYLKAOPSPKGPYV 526
 QY 429 VENIGYKVTITWKEIKPSEKGIICNTTIFYOAGGKGFKYVNSSILIOYGLES.LKRT 488
 Db 527 TKVYGNEAVLEMDQLPVDVQNGFTRNTTIFRTILIGETAVVNDSSHTEYTLSSLSDT 586
 QY 489 SYIVQYASTSAGTNGTSINFKLSFVSFEIILTSLIGGLILLILTVAYGLKKRP 548
 Db 587 LYVMRAAATDEGCKGKGPEFTPTPKFQAGEIATVAVCVLAFLLTLGLVLCFNKRL 646
 QY 549 LTHLCWPTYNPASTSIATW-----HGDPFKKL 577
 Db 647 IKHIMPVNDPSKSHIAQWSPHTPRHNENSKDM 682

RESULT 6
 US-09-455-962-2
 Sequence 2, Application US/09455962
 Patent No. 6524817
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/455, 962
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/058, 264
 FILING DATE:
 APPLICATION NUMBER: US 08/249, 553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 708 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-455-962-2

Query Match 17.4%; Score 678.5; DB 4; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKENISCYVYKKNLTCTSPGKETS-ITYVK---RYAGE---KHD---NCTN 71
DB 126 PEKRNLSICVINECKKMCCEWDGGRTHLETFNLKSEMAHFKPADKAKNDPTSCVD 185
QY 72 SSTENRASCFFLPRTIPDNTIYEAEAGDGVKS-HMTYRLENIAKTEPPKIFRY 130
DB 186 YST-----YFV-----NIEWWEAENALCKVSDHNFDPYK-V-KPNPHNLV 230
QY 131 KPVLGIRKMIQIEIKPELAVSSDLKYLTFRTVNSTWMEVFNARRKDKNOTYMLTG 190
DB 231 INSEELSLIKLTWTNPSIKSVII-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288
QY 191 LQPTTEVYIALRCVAVKESK-FWSDMSOEKMGTEEEAPC-GLELMRYLKPRAEAGRRPV 248
DB 289 LKPTTEVYFIRCKMEKDGKGYSDWSEASGITIEDRSKAPSFWKIDPSHTQGYRTVQ 348
QY 249 LLMKARGAPYLEKTLGYNIMYPESTNLTETMNTTNOQLEHLIGSEFVMSISYNSL 308
DB 349 LVMKTLRPFEEANGKILDEYVLTTRMKSHLQNTYVNAI--KLTVALINDRYLATITLVRLV 406
QY 309 GKSPVATLRIPAIQESFCIEVQAQVAEDQLVYKQSSALDVNTWMIEMFPDVSEPT 368
DB 407 GKSDAAVLTIPACDFQATHPVMDLKAPKDNMLWEMTTPRESVKYKYLEWCVLSDKAPC 466
QY 369 TLSMESVQAATNMTIQQDKLKPFCYNISVYPMHDKVGEYSIQAVAKESVPSGEPETK 428
DB 467 ITDWOQEDGVHRTYLRGNLAESKCYLITVPVADGSPESIKAYLKQAPSPKGPVVR 526
QY 429 VENIGVKVTITWKEIPKSEKGIICNTIIFYQAEKGFGFKTJNSILOGLESILKRT 488
DB 527 TKYKGNNAVLEMOQLPVDVONGFIRNTITIRTLIGMETAVNDSSTETETLSLSDT 586
QY 489 SYIVQVMASTAGTNGTSINFKTLSEVFEIILITSLIGGLLILLLVAVGLKPNK 548
DB 587 LYVWMAAYTDEGGDGEFTFTPKFAOGEIEAIVPVCLAFLLTLLGLVFCFNKDL 646
QY 549 LTHLCWTPVNPAAESTATW-----HGDDFKDL 577
DB 647 IKKHWPVNPDPKSHIAQWSPHPPRRHNFNSKDOM 682

RESULT 7
PCT-US95-06530-2

Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match 17.4%; Score 678.5; DB 5; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKENISCYVYKKNLTCTSPGKETS-ITYVK---RYAGE---KHD---NCTN 71
DB 126 PEKRNLSICVINECKKMCCEWDGGRTHLETFNLKSEMAHFKPADKAKNDPTSCVD 185
QY 72 SSTENRASCFFLPRTIPDNTIYEAEAGDGVKS-HMTYRLENIAKTEPPKIFRY 130
DB 186 YST-----YFV-----NIEWWEAENALCKVSDHNFDPYK-V-KPNPHNLV 230
QY 131 KPVLGIRKMIQIEIKPELAVSSDLKYLTFRTVNSTWMEVFNARRKDKNOTYMLTG 190
DB 231 INSEELSLIKLTWTNPSIKSVII-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288
QY 191 LQPTTEVYIALRCVAVKESK-FWSDMSOEKMGTEEEAPC-GLELMRYLKPRAEAGRRPV 248
DB 289 LKPTTEVYFIRCKMEKDGKGYSDWSEASGITIEDRSKAPSFWKIDPSHTQGYRTVQ 348
QY 249 LLMKARGAPYLEKTLGYNIMYPESTNLTETMNTTNOQLEHLIGSEFVMSISYNSL 308
DB 349 LVMKTLRPFEEANGKILDEYVLTTRMKSHLQNTYVNAI--KLTVALINDRYLATITLVRLV 406
QY 309 GKSPVATLRIPAIQESFCIEVQAQVAEDQLVYKQSSALDVNTWMIEMFPDVSEPT 368
DB 407 GKSDAAVLTIPACDFQATHPVMDLKAPKDNMLWEMTTPRESVKYKYLEWCVLSDKAPC 466
QY 369 TLSMESVQAATNMTIQQDKLKPFCYNISVYPMHDKVGEYSIQAVAKESVPSGEPETK 428
DB 467 ITDWOQEDGVHRTYLRGNLAESKCYLITVPVADGSPESIKAYLKQAPSPKGPVVR 526
QY 429 VENIGVKVTITWKEIPKSEKGIICNTIIFYQAEKGFGFKTJNSILOGLESILKRT 488
DB 527 TKYKGNNAVLEMOQLPVDVONGFIRNTITIRTLIGMETAVNDSSTETETLSLSDT 586
QY 489 SYIVQVMASTAGTNGTSINFKTLSEVFEIILITSLIGGLLILLLVAVGLKPNK 548
DB 587 LYVWMAAYTDEGGDGEFTFTPKFAOGEIEAIVPVCLAFLLTLLGLVFCFNKDL 646
QY 549 LTHLCWTPVNPAAESTATW-----HGDDFKDL 577
DB 647 IKKHWPVNPDPKSHIAQWSPHPPRRHNFNSKDOM 682

RESULT 8

US-08-825-558-6
Sequence 6, Application US/08825558
Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW

Db 349 LWMKLPPEFANGKILDEYVTLTRMKSHLQNTVNAAT--KLTVNLTDNDRYLATLTVRLV 406
Qy 309 GKSPVATLRLPAIDKESQCLLEVWQACAEQOLVYKKQSSALDVNTWMIEMFPDVSDEPT 368
Db 407 GKSDAAVLTTPACDFQATHPMDLKAFPKDMLWEMWTPPRESVKKYILLECVLSDAKPC 466
Qy 369 TLMSEVSQATNMWITQODKLPFCWCYNISVYPMLDKVGEPYSIOAVAKEGVSPSEGETK 428
Db 467 ITDMQOEDGYHRIYKLNLAESKCYLITVPYVADGSPESIKAYIKOAPPSKGPTR 526
Qy 429 VENIGKVTITWKEIPKSEKGIICNTYTFYQAEQKFSKTVNSSILOGLSLKRT 488
Db 527 TKVGNKNAVLEMDQLPVDQNGEIRNYTIFRYTIGNETAVNDSHTEYLSLSDT 586
Qy 489 SYIVQVMASTAGTNGTSINFKLSFVFELIITSLIGGLLILITVAYGLKRNK 548
Db 587 LYVWMAVYDEGKGDEFTTTPKFAQGEIEALVVPCLAFLLITLGLVFCFNKDL 646
Qy 549 LTHLWPTVPNPAESSIATW-----HGDDFKDL----- 577
Db 647 IKHIMVWPDPSPKSHLQWSPHPPRHNFSKQMSDGNFTDVSVEIEANDKKRPE 706
Qy 578 NLKESD---DSVNT 589
Db 707 DLKSLDLFKKKEKINTE 722

RESULT 10
US-09-313-942-9

Sequence 9, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 951
TYPE: PRT
ORGANISM: Homo sapiens
US-09-313-942-9

Query Match 16.1%; Score 629; DB 4; Length 951;

Best Local Similarity 26.7%; Pred. No. 8.7e-50;

Matches 193; Conservative 113; Mismatches 286; Indels 132; Gaps 26;

Qy 22 PAKPENISCVYYRRKNLCTWSPGKESY--TOYVYK---RYRAGE---KHD---NCTN 71
Db 126 PEKRNLSCLIVNEGKMKCEMDGGRHLETFNLKSEWATHKRFDCAKADPTSCVD 185
Qy 72 STSENRASSCFLLPRITIPNYTLEVENGDVYKS--HMYWLENIARTPEPKIPRY 130
Db 186 YST-----YFV-----NIEVWEAENALGVTSDHINFDVYAV--KPNPHNLSV 230
Qy 131 KPVIGIKMIOIEMTKPELAVYSSDLKTLRFYVNSTSMKEVNAKRRKDKNOTYNLGT 190
Db 231 INSELSLILKLTWNPISKSVII--LKYNIOYRTDASTWQIP--PEDTASTRSSFTVD 288
Qy 191 LOPFTEYIALRCAYKESK--FMSDMSQKMGTEEEAPC--GLELMRVLKPAEADGRPRV 248
Db 289 LKPFLEYFRIRCKMDEKGTWSDSEASGITTEDRSKAPSEFYKIDPSTQGYRVO 348
Qy 249 LLMKARGAPVLEKTLGINIWIYYPESNTNLTETNMNTQOELHIGSEFWMSISYSL 308

Db 349 LWMKLPPEFANGKILDEYVTLTRMKSHLQNTVNAAT--KLTVNLTDNDRYLATLTVRLV 406
Qy 309 GKSPVATLRLPAIDKESQCLLEVWQACAEQOLVYKKQSSALDVNTWMIEMFPDVSDEPT 368
Db 407 GKSDAAVLTTPACDFQATHPMDLKAFPKDMLWEMWTPPRESVKKYILLECVLSDAKPC 466
Qy 369 TLMSEVSQATNMWITQODKLPFCWCYNISVYPMLDKVGEPYSIOAVAKEGVSPSEGETK 428
Db 467 ITDMQOEDGYHRIYKLNLAESKCYLITVPYVADGSPESIKAYIKOAPPSKGPTR 526
Qy 429 VENIGKVTITWKEIPKSEKGIICNTYTFYQAEQKFSKTVNSSILOGLSLKRT 488
Db 527 TKVGNKNAVLEMDQLPVDQNGEIRNYTIFRYTIGNETAVNDSHTEYLSLSDT 586
Qy 489 SYIVQVMASTAGTNGTSINFKLSFVFELIITSLIGGLLILITVAYGLKRNK 548
Db 587 LYVWMAVYDEGKGDEFTTTPKFAQGEIEGASTKGSVPLADSSKSGGYAAL 646
Qy 535 IILVAYGLKRNKLTHLWPTVPNPAESSIATWHDGDFKDLN-----LKE----- 582
Db 647 GCLVKDY-----PEPYTVS---WNSGALTSGVHTFPAVLQSSGLYSLS 688
Qy 583 -----DSVNTEDRIL---KPCSTPSDKLVIDKLVWNGVLOEITFDEARTGOENNLG 633
Db 689 VVTVPSSSLGTQYICNVNHHKPSMTKVDKV-----EPKSCDKTH-- 728
Qy 634 GEKNQVTCPPRPDCLPSFEELPVSPET---PPR--KSQYLRSMPGT-----R 680
Db 729 -----TC---PCPA---PELLGGSVLEFPKPKDMLTISRTPEVTGVVVDVSHED 774
Qy 681 PEAK 684
Db 775 PEVK 778

RESULT 11
US-08-419-652-5

Sequence 5, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: CD 9174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-825-558-4

Query Match 15.8%; Score 618; DB 2; Length 658;

Best Local Similarity 28.9%; Pred. No. 5,1e-49;
Matches 156; Conservative 104; Mismatches 233; Indels 46; Gaps 15;

QY 22 PAKRENISCVYYKNNLCTWSPCKETSY--TOYTVK---RTYAGE---KHD---NCTTN 71
DB 126 PEKKNLSICVYNEGKMKRCCEWGGRETHLENTFLKSEMAHKFADCKARKDPTSTCTVD 185
QY 72 SSTEENRASCSEFLPRITPDNTIEVEAENGDAVIRS-HMTYRLKLENIKTEPKIFRY 130
DB 186 YST-----YEFV-----NIEWWEAENALGKVTSDHINFPYKVV-KPNPNNLSV 230
QY 131 KPVIGIKRMIOIEMIKPELAPVSSDLKYTLREFRVNSTSMWEVNFANRDKDKNOTYMLTG 190
DB 231 INSELSILKLTWNTNSIKSVII-LKYNIOYRTKDKASTWSQIP-PEDTASTRSSFTYOD 288
QY 191 LQPTTEVIALRCVAKESK-FWSDMSQKMGMTTEEPAPC-GLELMRYLKPALADGRPRVR 248
DB 289 LKPTTEVFRIKCKEDGKGYSDMSSEASGITVEDRSPKAPSFMYKIDPSHTOGYRTVQ 348
QY 249 LMKKAGAPVLEKTLGYNIMWYPESENTNLETMTNTNOOLEHLHGSEFVSMISYNSL 308
DB 349 LMKTLRPFPEANGKILDIYEVTLTRKSHLONTYVNAF-KLTYNLTNDRYLATLTVRNLV 406
QY 309 GKSPVATLRIPAIQESFQCIENVQACVAEDQVVKQSSALDVNTWMIEMFPVDSEPT 368
DB 407 GKSDAAVLTIPACFOQATHPYMDLKAFFPKDMLMVEWTPPRESVKYIILEKCVLSDAAPC 466
QY 369 TLSWESVSQATNWTIQDDKLRPFWCYNISVYPMJLHDKVGEYSIOAVAKEGVSEGPETK 428
DB 467 ITDWOEDGVTHRYLKGNIKLAESKCYLITVPYVADGSPESIKAYLKQAPSPKTPVR 526
QY 429 VENIGVTVITTWKEIKSERKGIICVNTTIFYQAEKGKFSKYVNSSILOGLGSLRKRT 488
DB 527 TKKVGKNAVLEMQOLPVDQNGFIRNTTIFYRTIIGNETAVNVDSSHTETLSSLSDT 586
QY 489 SYIVQVASTSAGTNGTSINFKT-----LSFSVFELIILTS---LIGGLLI 533
DB 587 LYMVMAAYTDEGKDGPEFTFTTPKPELKNTSGLMFOILORVILPSGHLTLLOGTILI 645

RESULT 14
US-09-312-611-4
Sequence 4, Application US/09312611
Patent No. 6380160

GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.

APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: GP130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-312-611-4

Query Match 15.8%; Score 618; DB 4; Length 658;

Best Local Similarity 28.9%; Pred. No. 5,1e-49;
Matches 156; Conservative 104; Mismatches 233; Indels 46; Gaps 15;

QY 22 PAKRENISCVYYKNNLCTWSPCKETSY--TOYTVK---RTYAGE---KHD---NCTTN 71
DB 126 PEKKNLSICVYNEGKMKRCCEWGGRETHLENTFLKSEMAHKFADCKARKDPTSTCTVD 185
QY 72 SSTEENRASCSEFLPRITPDNTIEVEAENGDAVIRS-HMTYRLKLENIKTEPKIFRY 130
DB 186 YST-----YEFV-----NIEWWEAENALGKVTSDHINFPYKVV-KPNPNNLSV 230
QY 131 KPVIGIKRMIOIEMIKPELAPVSSDLKYTLREFRVNSTSMWEVNFANRDKDKNOTYMLTG 190
DB 231 INSELSILKLTWNTNSIKSVII-LKYNIOYRTKDKASTWSQIP-PEDTASTRSSFTYOD 288
QY 191 LQPTTEVIALRCVAKESK-FWSDMSQKMGMTTEEPAPC-GLELMRYLKPALADGRPRVR 248
DB 289 LKPTTEVFRIKCKEDGKGYSDMSSEASGITVEDRSPKAPSFMYKIDPSHTOGYRTVQ 348
QY 249 LMKKAGAPVLEKTLGYNIMWYPESENTNLETMTNTNOOLEHLHGSEFVSMISYNSL 308
DB 349 LMKTLRPFPEANGKILDIYEVTLTRKSHLONTYVNAF-KLTYNLTNDRYLATLTVRNLV 406
QY 309 GKSPVATLRIPAIQESFQCIENVQACVAEDQVVKQSSALDVNTWMIEMFPVDSEPT 368
DB 407 GKSDAAVLTIPACFOQATHPYMDLKAFFPKDMLMVEWTPPRESVKYIILEKCVLSDAAPC 466
QY 369 TLSWESVSQATNWTIQDDKLRPFWCYNISVYPMJLHDKVGEYSIOAVAKEGVSEGPETK 428
DB 467 ITDWOEDGVTHRYLKGNIKLAESKCYLITVPYVADGSPESIKAYLKQAPSPKTPVR 526
QY 429 VENIGVTVITTWKEIKSERKGIICVNTTIFYQAEKGKFSKYVNSSILOGLGSLRKRT 488
DB 527 TKKVGKNAVLEMQOLPVDQNGFIRNTTIFYRTIIGNETAVNVDSSHTETLSSLSDT 586
QY 489 SYIVQVASTSAGTNGTSINFKT-----LSFSVFELIILTS---LIGGLLI 533
DB 587 LYMVMAAYTDEGKDGPEFTFTTPKPELKNTSGLMFOILORVILPSGHLTLLOGTILI 645

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:15:41 ; Search time 28 Seconds
(without alignments)
3104.720 Million cell updates/sec

Title: US-09-892-949-2

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Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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18: /cgn2-6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3896	99.7	745	11	US-09-972-708-4
3	3405.5	87.1	649	11	US-09-892-949-46
4	3405.5	87.1	662	11	US-09-972-708-15
5	3405.5	87.1	662	11	US-09-892-949-54
6	3405.5	87.1	662	15	US-10-006-265-17
7	3350	85.7	652	11	US-09-972-708-14
8	3350	85.7	652	15	US-10-006-265-2
9	2783	71.2	764	11	US-09-892-949-69
10	2546	65.1	582	15	US-10-230-163-92
11	2546	65.1	582	15	US-10-230-338-92
12	2546	65.1	582	15	US-10-218-631-92
13	2546	65.1	582	15	US-10-230-414-92
14	2546	65.1	582	15	US-10-216-159A-92
15	2546	65.1	582	15	US-10-216-159A-92

16	2546	65.1	582	15	US-10-218-849-92	Sequence 92, Appl
17	2546	65.1	582	15	US-10-227-873-92	Sequence 92, Appl
18	2546	65.1	582	15	US-10-227-883-92	Sequence 92, Appl
19	2546	65.1	582	15	US-10-219-076-92	Sequence 92, Appl
20	2546	65.1	582	15	US-10-230-434-92	Sequence 92, Appl
21	2546	65.1	582	15	US-10-219-003-92	Sequence 92, Appl
22	2546	65.1	582	15	US-10-219-075-92	Sequence 92, Appl
23	2546	65.1	582	15	US-10-219-464-92	Sequence 92, Appl
24	2546	65.1	582	15	US-10-219-466-92	Sequence 92, Appl
25	2546	65.1	582	15	US-10-219-479-92	Sequence 92, Appl
26	2546	65.1	582	15	US-10-219-481-92	Sequence 92, Appl
27	2546	65.1	582	15	US-10-230-260-92	Sequence 92, Appl
28	2546	65.1	582	15	US-10-232-231-92	Sequence 92, Appl
29	2546	65.1	582	15	US-10-232-233-92	Sequence 92, Appl
30	2546	65.1	582	15	US-10-216-165-92	Sequence 92, Appl
31	2546	65.1	582	15	US-10-218-956-92	Sequence 92, Appl
32	2546	65.1	582	15	US-10-219-468-92	Sequence 92, Appl
33	2546	65.1	582	15	US-10-219-478-92	Sequence 92, Appl
34	2546	65.1	582	15	US-10-219-536-92	Sequence 92, Appl
35	2546	65.1	582	15	US-10-233-205-92	Sequence 92, Appl
36	2546	65.1	582	15	US-10-219-072-92	Sequence 92, Appl
37	2546	65.1	582	15	US-10-219-470-92	Sequence 92, Appl
38	2546	65.1	582	15	US-10-219-474-92	Sequence 92, Appl
39	2546	65.1	582	15	US-10-219-524-92	Sequence 92, Appl
40	2546	65.1	582	15	US-10-219-528-92	Sequence 92, Appl
41	2546	65.1	582	15	US-10-227-880-92	Sequence 92, Appl
42	2546	65.1	582	15	US-10-227-881-92	Sequence 92, Appl
43	2546	65.1	582	15	US-10-227-882-92	Sequence 92, Appl
44	2546	65.1	582	15	US-10-230-436-92	Sequence 92, Appl
45	2546	65.1	582	15	US-10-232-223-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1
US-09-892-949-2
Sequence 2, Application US/09892949.
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprechel, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuiper, Joseph L.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 732
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-949-2

Query Match 100.0%; Score 3908; DB 11; Length 732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTWALMLPISLCKFSLAAIPAKPENISCVYYRKNTCTWWSCKEYSTYQYVKKRYA 60
DB 1 MMTWALMLPISLCKFSLAAIPAKPENISCVYYRKNTCTWWSCKEYSTYQYVKKRYA 60
QY 61 FGEKHNDCTNNTSENRAKSCFFLPRTIPDNTIEVEAENGCVIKSHMTWRLLENIA 120

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Db 61 FGEKDNCTNNTSSSENBRASCFFLPRTITPDNTYEVEAENGDCVISHMTYMLNIA 120
Qy 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKAKRK 180
Db 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKAKRK 180
Qy 181 DKNQTYNLTLGLOPFEYVIALRCAYKESKFMSDSQEMKGMT EEPAPCGLEIMRLKPAE 240
Db 181 DKNQTYNLTLGLOPFEYVIALRCAYKESKFMSDSQEMKGMT EEPAPCGLEIMRLKPAE 240
Qy 241 ADGRPRVRLMKKAGAVLEKTLGYNIMYYPESNTNLTETMNTNNOOLEHLGSESPV 300
Db 241 ADGRPRVRLMKKAGAVLEKTLGYNIMYYPESNTNLTETMNTNNOOLEHLGSESPV 300
Qy 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDQLVKQSSALDYNMTMIMF 360
Db 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDQLVKQSSALDYNMTMIMF 360
Qy 361 PDVDEPTTLMESVSQATNMTIQQDKLPFCYNISSVYPMHLKVGEPYSIOAYAKBGV 420
Db 361 PDVDEPTTLMESVSQATNMTIQQDKLPFCYNISSVYPMHLKVGEPYSIOAYAKBGV 420
Qy 421 PSEGETVENINGVTVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 480
Db 421 PSEGETVENINGVTVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 480
Qy 481 LESLKRKTSYIVQWASTSAGTNGTSINFKTLSPVEIILITSLIGGLILITLVA 540
Db 481 LESLKRKTSYIVQWASTSAGTNGTSINFKTLSPVEIILITSLIGGLILITLVA 540
Qy 541 YGLKPKNLTLHLCWPTVPNPAESSIATWHGDFKDKLNLKESDSDSVNTERILKPCSTPS 600
Db 541 YGLKPKNLTLHLCWPTVPNPAESSIATWHGDFKDKLNLKESDSDSVNTERILKPCSTPS 600
Qy 601 DKLVIDKLVNFGNVLQEIFTDEARTGOENNLGCKNGYVTCPPRPDCPLKSEELPVS 660
Db 601 DKLVIDKLVNFGNVLQEIFTDEARTGOENNLGCKNGYVTCPPRPDCPLKSEELPVS 660
Qy 661 PEIPPRKSOYLRSRMPBSTREPAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 720
Db 661 PEIPPRKSOYLRSRMPBSTREPAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 720
Qy 721 SEKLPEHTKGEV 732
Db 721 SEKLPEHTKGEV 732

RESULT 2
US-09-972-708-4
: Sequence 4, Application US/09972708
: Publication No. US20030059871A1
: GENERAL INFORMATION:
: APPLICANT: Immunex Corporation
: APPLICANT: Cosman, David J.
: APPLICANT: Mosley, Bruce A.
: APPLICANT: Bird, Timothy A.
: APPLICANT: Dubose, Robert F.
: APPLICANT: Wiley, Steven R.
: TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
: FILE REFERENCE: 3160-B
: CURRENT APPLICATION NUMBER: US/09/972.708
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 745
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-708-4

Query Match 99.7%; Score 3896; DB 11: Length 745;
Best Local Similarity 99.7%; Pred. No. 0;
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Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MMWTALMLPDLCKFSALAPAKPENISCYYYKKNLTCTMSPCKESTYQYTKRYA 60
Db 14 MMWTALMLPDLCKFSALAPAKPENISCYYYKKNLTCTMSPCKESTYQYTKRYA 73
Qy 61 FGEKDNCTNNTSSSENBRASCFFLPRTITPDNTYEVEAENGDCVISHMTYMLNIA 120
Db 74 FGEKDNCTNNTSSSENBRASCFFLPRTITPDNTYEVEAENGDCVISHMTYMLNIA 133
Qy 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKAKRK 180
Db 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKAKRK 193
Qy 181 DKNQTYNLTLGLOPFEYVIALRCAYKESKFMSDSQEMKGMT EEPAPCGLEIMRLKPAE 240
Db 181 DKNQTYNLTLGLOPFEYVIALRCAYKESKFMSDSQEMKGMT EEPAPCGLEIMRLKPAE 253
Qy 241 ADGRPRVRLMKKAGAVLEKTLGYNIMYYPESNTNLTETMNTNNOOLEHLGSESPV 300
Db 241 ADGRPRVRLMKKAGAVLEKTLGYNIMYYPESNTNLTETMNTNNOOLEHLGSESPV 313
Qy 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDQLVKQSSALDYNMTMIMF 360
Db 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDQLVKQSSALDYNMTMIMF 373
Qy 361 PDVDEPTTLMESVSQATNMTIQQDKLPFCYNISSVYPMHLKVGEPYSIOAYAKBGV 420
Db 361 PDVDEPTTLMESVSQATNMTIQQDKLPFCYNISSVYPMHLKVGEPYSIOAYAKBGV 433
Qy 421 PSEGETVENINGVTVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 480
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Qy 661 PEIPPRKSOYLRSRMPBSTREPAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 720
Db 661 PEIPPRKSOYLRSRMPBSTREPAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 733
Qy 721 SEKLPEHTKGEV 732
Db 721 SEKLPEHTKGEV 745

RESULT 3
US-09-892-949-46
: Sequence 46, Application US/09892949
: Publication No. US20030096339A1
: GENERAL INFORMATION:
: APPLICANT: Sprechet, Cindy A.
: APPLICANT: Presnell, Scott R.
: APPLICANT: Geo. Zeren
: APPLICANT: Whitmore, Theodore E.
: APPLICANT: Kuiper, Joseph L.
: APPLICANT: Maurer, Mark F.
: TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
: FILE REFERENCE: 00-42
: CURRENT APPLICATION NUMBER: US/09/892.949
: PRIOR APPLICATION NUMBER: US 60/214,282
: PRIOR FILING DATE: 2000-06-26
: PRIOR APPLICATION NUMBER: US 60/214,955
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;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: US 60/267,963
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ. ID NOS: 93
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 46
;; LENGTH: 649
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-892-949-46

Query Match 87.1%; Score 3405.5; DB 11; Length 649;
Best Local Similarity 99.1%; Pred. No. 5.2e-291;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

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DB 61 FGEKHNCTNNSSESRASCSEFLPRITIPDNNTIEVEANGDGVKSHMTWRLNIA 120
QY 121 KTEPPKIFRYKPYLGIRMIQIEMIKELAPVSSDLKYLRFRTVNSTSMMEVFAKNRK 180
DB 121 KTEPPKIFRYKPYLGIRMIQIEMIKELAPVSSDLKYLRFRTVNSTSMMEVFAKNRK 180
QY 181 DKNOTYVLTGLOPTEVIALRCVAVKESKWSQKMGTEBEAPCGLELRVLPKPAE 240
DB 181 DKNOTYVLTGLOPTEVIALRCVAVKESKWSQKMGTEBEAPCGLELRVLPKPAE 240
QY 241 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMNTNOQLHIGSEFW 300
DB 241 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMNTNOQLHIGSEFW 300
QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVADOLVYKMOSSALDVNTMIEMF 360
DB 301 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVADOLVYKMOSSALDVNTMIEMF 360
QY 361 PDVDSERTTSLMESVSQATWMTTQODKLPFCWCNISVYPMLDKVGEPISQAYAKEGV 420
DB 361 PDVDSERTTSLMESVSQATWMTTQODKLPFCWCNISVYPMLDKVGEPISQAYAKEGV 420
QY 421 PSEGPETKVENIGKVTYITWKEIPKSERGIICNTYIFQAEGBGKFSKTVNSSIIQYG 480
DB 421 PSEGPETKVENIGKVTYITWKEIPKSERGIICNTYIFQAEGBGKFSKTVNSSIIQYG 480
QY 481 LESLKRTSYIVOMASTSAGTNGTSINFKTLSFSVFEIILITSLIGGILLIILTV 540
DB 481 LESLKRTSYIVOMASTSAGTNGTSINFKTLSFSVFEIILITSLIGGILLIILTV 540
QY 541 YGLKRPKRLHLCPYTPNPAESSIATWHDDEKDKLNKESDSDSVTEBRILKPCSTPS 600
DB 541 YGLKRPKRLHLCPYTPNPAESSIATWHDDEKDKLNKESDSDSVTEBRILKPCSTPS 600
QY 601 DKLVIDLVNFGNVLOEIFTDEARTQENNLGGEKNG---YVTCF 643
DB 601 DKLVIDLVNFGNVLOEIFTDEARTQENNLGGEKNGTRILSSCP 646

RESULT 4
US-09-972-708-15
;; Sequence 15; Application US/09972708
;; Publication NO. US2003005987A1
;; GENERAL INFORMATION:
;; APPLICANT: Immunex Corporation
;; APPLICANT: Cosman, David J.
;; APPLICANT: Mosley, Bruce A.
;; APPLICANT: Bird, Timothy A.
;; APPLICANT: Dubose, Robert F.
;; APPLICANT: Wiley, Steven R.
;; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
;; FILE REFERENCE: 3160-B

;; CURRENT APPLICATION NUMBER: US/09/972,708
;; CURRENT FILING DATE: 2001-10-05
;; NUMBER OF SEQ. ID NOS: 29
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 15
;; LENGTH: 662
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-972-708-15

Query Match 87.1%; Score 3405.5; DB 11; Length 662;
Best Local Similarity 99.1%; Pred. No. 5.3e-291;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 MMTWALMLPSCKSLALPAKPNISCVYYRRKLTCTWSPGKSTYTQTVKRTYA 60
DB 14 MMTWALMLPSCKSLALPAKPNISCVYYRRKLTCTWSPGKSTYTQTVKRTYA 73
QY 61 FGEKHNCTNNSSESRASCSEFLPRITIPDNNTIEVEANGDGVKSHMTWRLNIA 120
DB 74 FGEKHNCTNNSSESRASCSEFLPRITIPDNNTIEVEANGDGVKSHMTWRLNIA 133
QY 121 KTEPPKIFRYKPYLGIRMIQIEMIKELAPVSSDLKYLRFRTVNSTSMMEVFAKNRK 180
DB 134 KTEPPKIFRYKPYLGIRMIQIEMIKELAPVSSDLKYLRFRTVNSTSMMEVFAKNRK 193
QY 181 DKNOTYVLTGLOPTEVIALRCVAVKESKWSQKMGTEBEAPCGLELRVLPKPAE 240
DB 194 DKNOTYVLTGLOPTEVIALRCVAVKESKWSQKMGTEBEAPCGLELRVLPKPAE 253
QY 241 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMNTNOQLHIGSEFW 300
DB 254 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMNTNOQLHIGSEFW 313
QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVADOLVYKMOSSALDVNTMIEMF 360
DB 314 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVADOLVYKMOSSALDVNTMIEMF 373
QY 361 PDVDSERTTSLMESVSQATWMTTQODKLPFCWCNISVYPMLDKVGEPISQAYAKEGV 420
DB 374 PDVDSERTTSLMESVSQATWMTTQODKLPFCWCNISVYPMLDKVGEPISQAYAKEGV 433
QY 421 PSEGPETKVENIGKVTYITWKEIPKSERGIICNTYIFQAEGBGKFSKTVNSSIIQYG 480
DB 434 PSEGPETKVENIGKVTYITWKEIPKSERGIICNTYIFQAEGBGKFSKTVNSSIIQYG 493
QY 481 LESLKRTSYIVOMASTSAGTNGTSINFKTLSFSVFEIILITSLIGGILLIILTV 540
DB 494 LESLKRTSYIVOMASTSAGTNGTSINFKTLSFSVFEIILITSLIGGILLIILTV 553
QY 541 YGLKRPKRLHLCPYTPNPAESSIATWHDDEKDKLNKESDSDSVTEBRILKPCSTPS 600
DB 554 YGLKRPKRLHLCPYTPNPAESSIATWHDDEKDKLNKESDSDSVTEBRILKPCSTPS 613
QY 601 DKLVIDLVNFGNVLOEIFTDEARTQENNLGGEKNG---YVTCF 643
DB 614 DKLVIDLVNFGNVLOEIFTDEARTQENNLGGEKNGTRILSSCP 659

RESULT 5
US-09-892-949-54
;; Sequence 54; Application US/09892949
;; Publication NO. US2003009639A1
;; GENERAL INFORMATION:
;; APPLICANT: Sprechel, Cindy A.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Gao, Zeren
;; APPLICANT: Whitmore, Theodore E.
;; APPLICANT: Kuijper, Joseph L.
;; APPLICANT: Maurer, Mark F.
;; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
;; FILE REFERENCE: 00-42
;; CURRENT APPLICATION NUMBER: US/09/892,949

```
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 54
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-54
```

```
Query Match      87.1%; Score 3405.5; DB 11; Length 662:
Best Local Similarity 99.1%; Pred. No. 5.3e-291;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
```

```
OY 1 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 60
    |||||||
DB 14 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 73
    |||||||
OY 61 FGEKHDNCTNSTSENKASCSFLLPRTIPDNTTIEVEANGGVKSHMTYRLNIA 120
    |||||||
DB 74 FGEKHDNCTNSTSENKASCSFLLPRTIPDNTTIEVEANGGVKSHMTYRLNIA 133
    |||||||
OY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKYTLFRTVNSTSMVEVFAKRRK 180
    |||||||
DB 134 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKYTLFRTVNSTSMVEVFAKRRK 193
    |||||||
OY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSMDSOEKMGMTEBAPCGLEMLVLPKPAE 240
    |||||||
DB 194 DKNOTYNTGLQPTFEYVIALRCVAKESKFSMDSOEKMGMTEBAPCGLEMLVLPKPAE 253
    |||||||
OY 241 ADGRPRVRLMKKARGAVLEKTLGYNIWYPPESNTNLTETMNTTNOQLHLGEGSPFW 300
    |||||||
DB 254 ADGRPRVRLMKKARGAVLEKTLGYNIWYPPESNTNLTETMNTTNOQLHLGEGSPFW 313
    |||||||
OY 301 SMISYNSLGKSPVATLRIPALOEKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEWF 360
    |||||||
DB 314 SMISYNSLGKSPVATLRIPALOEKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEWF 373
    |||||||
OY 361 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 420
    |||||||
DB 374 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 433
    |||||||
OY 421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEKGKFSKTVNSSILOYG 480
    |||||||
DB 434 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEKGKFSKTVNSSILOYG 493
    |||||||
OY 481 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPFSVEIILLTSLIGGGLILLITLVA 540
    |||||||
DB 494 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPFSVEIILLTSLIGGGLILLITLVA 553
    |||||||
OY 541 YGLKPKMLTHLCPTVPNPAESSIATWHGDDFKDKLNLKESDVSNTEDRIILKPCSTPS 600
    |||||||
DB 554 YGLKPKMLTHLCPTVPNPAESSIATWHGDDFKDKLNLKESDVSNTEDRIILKPCSTPS 613
    |||||||
OY 601 DKLVIDKLVNFGVNLQEIFTDEARTGOENNLGEGKNG---YVYCP 643
    |||||||
DB 614 DKLVIDKLVNFGVNLQEIFTDEARTGOENNLGEGKNGTRLISCP 659
    |||||||
```

```
RESULT 6
US-10-006-265-17
; Sequence 17, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
```

```
; CURRENT APPLICATION NUMBER: US/10/006,265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 17
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-17
```

```
Query Match      87.1%; Score 3405.5; DB 15; Length 662:
Best Local Similarity 99.1%; Pred. No. 5.3e-291;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
```

```
OY 1 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 60
    |||||||
DB 14 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 73
    |||||||
OY 61 FGEKHDNCTNSTSENKASCSFLLPRTIPDNTTIEVEANGGVKSHMTYRLNIA 120
    |||||||
DB 74 FGEKHDNCTNSTSENKASCSFLLPRTIPDNTTIEVEANGGVKSHMTYRLNIA 133
    |||||||
OY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKYTLFRTVNSTSMVEVFAKRRK 180
    |||||||
DB 134 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKYTLFRTVNSTSMVEVFAKRRK 193
    |||||||
OY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSMDSOEKMGMTEBAPCGLEMLVLPKPAE 240
    |||||||
DB 194 DKNOTYNTGLQPTFEYVIALRCVAKESKFSMDSOEKMGMTEBAPCGLEMLVLPKPAE 253
    |||||||
OY 241 ADGRPRVRLMKKARGAVLEKTLGYNIWYPPESNTNLTETMNTTNOQLHLGEGSPFW 300
    |||||||
DB 254 ADGRPRVRLMKKARGAVLEKTLGYNIWYPPESNTNLTETMNTTNOQLHLGEGSPFW 313
    |||||||
OY 301 SMISYNSLGKSPVATLRIPALOEKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEWF 360
    |||||||
DB 314 SMISYNSLGKSPVATLRIPALOEKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEWF 373
    |||||||
OY 361 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 420
    |||||||
DB 374 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 433
    |||||||
OY 421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEKGKFSKTVNSSILOYG 480
    |||||||
DB 434 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEKGKFSKTVNSSILOYG 493
    |||||||
OY 481 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPFSVEIILLTSLIGGGLILLITLVA 540
    |||||||
DB 494 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPFSVEIILLTSLIGGGLILLITLVA 553
    |||||||
OY 541 YGLKPKMLTHLCPTVPNPAESSIATWHGDDFKDKLNLKESDVSNTEDRIILKPCSTPS 600
    |||||||
DB 554 YGLKPKMLTHLCPTVPNPAESSIATWHGDDFKDKLNLKESDVSNTEDRIILKPCSTPS 613
    |||||||
OY 601 DKLVIDKLVNFGVNLQEIFTDEARTGOENNLGEGKNG---YVYCP 643
    |||||||
DB 614 DKLVIDKLVNFGVNLQEIFTDEARTGOENNLGEGKNGTRLISCP 659
    |||||||
```

```
RESULT 7
US-09-972-708-14
; Sequence 14, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
```

APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972.708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 652
TYPE: PR
ORGANISM: Homo sapiens
US-09-972-708-14

Query Match 85.7%; Score 3350; DB 11; Length 652;
Best Local Similarity 99.8%; Pred. No. 4e-286;
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWTALMMLPSLCKFSLALPAKPENISCVYYRRKMLCTWSPGKETSTYQYVKKRYA 60
DB 14 MMWTALMMLPSLCKFSLALPAKPENISCVYYRRKMLCTWSPGKETSTYQYVKKRYA 73
QY 61 FGEKHDNCTNSTSENASCSEFLPRITTPDNTTIEVEANGDGVKSHMTYRLNIA 120
DB 74 FGEKHDNCTNSTSENASCSEFLPRITTPDNTTIEVEANGDGVKSHMTYRLNIA 133
QY 121 KTEPKIFRYKPVIGIRMIQIEMIKPELAVSSDLKYTLFRFVNSTSWMEVFAFNK 180
DB 134 KTEPKIFRYKPVIGIRMIQIEMIKPELAVSSDLKYTLFRFVNSTSWMEVFAFNK 193
QY 181 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLP 240
DB 194 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLP 253
QY 241 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSEFW 300
DB 254 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSEFW 313
QY 301 SMISYNSLGSPVATLRIPAIQKSFQCI EYMAQVADOLVVKQSSALDVNTMTIEMF 360
DB 314 SMISYNSLGSPVATLRIPAIQKSFQCI EYMAQVADOLVVKQSSALDVNTMTIEMF 373
QY 361 PDVNSEPTLTSWESVSQATNMTIOODKLRPWCYNISYVPMHLHKVGEPPYSIOAYAREGV 420
DB 374 PDVNSEPTLTSWESVSQATNMTIOODKLRPWCYNISYVPMHLHKVGEPPYSIOAYAREGV 433
QY 421 PSEGPETKVENIGVKTYYITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSILOYG 480
DB 434 PSEGPETKVENIGVKTYYITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSILOYG 493
QY 481 LESLKRKTSYIVQYMASTAGCTNGTSTINFTLSFSVEIILLITSLIGGGLIIILITVA 540
DB 494 LESLKRKTSYIVQYMASTAGCTNGTSTINFTLSFSVEIILLITSLIGGGLIIILITVA 553
QY 541 YGLKKPKNLHLCPYTPNPRESSIATWHDGDFDKMLAKESDSDSVNTEDEILKPCSTPS 600
DB 554 YGLKKPKNLHLCPYTPNPRESSIATWHDGDFDKMLAKESDSDSVNTEDEILKPCSTPS 613
QY 601 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 629
DB 614 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 642

RESULT 8
US-10-006-265-2
Sequence 2, Application US/10006265
Publication No. US20030125520A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001

CURRENT APPLICATION NUMBER: US/10/006.265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 652
TYPE: PR
ORGANISM: Homo sapiens
US-10-006-265-2

Query Match 85.7%; Score 3350; DB 15; Length 652;
Best Local Similarity 99.8%; Pred. No. 4e-286;
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWTALMMLPSLCKFSLALPAKPENISCVYYRRKMLCTWSPGKETSTYQYVKKRYA 60
DB 14 MMWTALMMLPSLCKFSLALPAKPENISCVYYRRKMLCTWSPGKETSTYQYVKKRYA 73
QY 61 FGEKHDNCTNSTSENASCSEFLPRITTPDNTTIEVEANGDGVKSHMTYRLNIA 120
DB 74 FGEKHDNCTNSTSENASCSEFLPRITTPDNTTIEVEANGDGVKSHMTYRLNIA 133
QY 121 KTEPKIFRYKPVIGIRMIQIEMIKPELAVSSDLKYTLFRFVNSTSWMEVFAFNK 180
DB 134 KTEPKIFRYKPVIGIRMIQIEMIKPELAVSSDLKYTLFRFVNSTSWMEVFAFNK 193
QY 181 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLP 240
DB 194 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLP 253
QY 241 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSEFW 300
DB 254 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSEFW 313
QY 301 SMISYNSLGSPVATLRIPAIQKSFQCI EYMAQVADOLVVKQSSALDVNTMTIEMF 360
DB 314 SMISYNSLGSPVATLRIPAIQKSFQCI EYMAQVADOLVVKQSSALDVNTMTIEMF 373
QY 361 PDVNSEPTLTSWESVSQATNMTIOODKLRPWCYNISYVPMHLHKVGEPPYSIOAYAREGV 420
DB 374 PDVNSEPTLTSWESVSQATNMTIOODKLRPWCYNISYVPMHLHKVGEPPYSIOAYAREGV 433
QY 421 PSEGPETKVENIGVKTYYITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSILOYG 480
DB 434 PSEGPETKVENIGVKTYYITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSILOYG 493
QY 481 LESLKRKTSYIVQYMASTAGCTNGTSTINFTLSFSVEIILLITSLIGGGLIIILITVA 540
DB 494 LESLKRKTSYIVQYMASTAGCTNGTSTINFTLSFSVEIILLITSLIGGGLIIILITVA 553
QY 541 YGLKKPKNLHLCPYTPNPRESSIATWHDGDFDKMLAKESDSDSVNTEDEILKPCSTPS 600
DB 554 YGLKKPKNLHLCPYTPNPRESSIATWHDGDFDKMLAKESDSDSVNTEDEILKPCSTPS 613
QY 601 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 629
DB 614 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 642

RESULT 9
US-09-892-949-69
Sequence 69, Application US/09892949
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren

APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuifer, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTORL7
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 69
LENGTH: 764
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human zcytorl7-Fc4 fusion polypeptide
us-09-892-949-69

Query Match 71.2%; Score 2783; DB 11; Length 764;
Best Local Similarity 93.8%; Pred. No. 4.6e-236;
Matches 525; Conservative 2; Mismatches 9; Indels 24; Gaps 2;

QY 1 MMTWALMLPLSLCKFSLAALPAKPENISCVYYRKNNLTGMSPEKENSYYQYVKKRYA 60
DB 14 MMTWALMLPLSLCKFSLAALPAKPENISCVYYRKNNLTGMSPEKENSYYQYVKKRYA 73
QY 61 FGEKHNDCTNSTSENASCSEFLPRITIPDNTYIEVEANGGVKSHMTYRLENIA 120
DB 74 FGEKHNDCTNSTSENASCSEFLPRITIPDNTYIEVEANGGVKSHMTYRLENIA 133
QY 121 KTEPKITFRVAVGIRKMIQIEMTKPELAYSSDLKTLFRVYNSISMHEVNAKRRK 180
DB 134 KTEPKITFRVAVGIRKMIQIEMTKPELAYSSDLKTLFRVYNSISMHEVNAKRRK 193
QY 181 DKNOTYNLTGQPTFEYVIALRCVAKESKFWSDMSOEKMGTEEPAPCGLEMLVLPKPAE 240
DB 194 DKNOTYNLTGQPTFEYVIALRCVAKESKFWSDMSOEKMGTEEPAPCGLEMLVLPKPAE 253
QY 241 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTLLETMTNTNOGLEHLGSESPV 300
DB 254 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTLLETMTNTNOGLEHLGSESPV 313
QY 301 SMIVYNSLGKSPVATLRIPATOEKSFQCIEMQACVAEDOLVVKWQSALDVNTWMIEMF 360
DB 314 SMIVYNSLGKSPVATLRIPATOEKSFQCIEMQACVAEDOLVVKWQSALDVNTWMIEMF 373
QY 361 PDVDEPTTSLMESVSQATNMTIQODKLPFWCYNISVYPMALHVKCEPYSIQAVAKEGV 420
DB 374 PDVDEPTTSLMESVSQATNMTIQODKLPFWCYNISVYPMALHVKCEPYSIQAVAKEGV 433
QY 421 PSEBPEKVENIGVYVTTTWKEIPKSEKGIICNYTIFYOAEKGKGSFTVNSSIIQYG 480
DB 434 PSEBPEKVENIGVYVTTTWKEIPKSEKGIICNYTIFYOAEKGKGSFTVNSSIIQYG 493
QY 481 LESLKRTSYIVQYMASTAGCTGNTSINFKTLSPFVFEILLITSLIGGLILLIILTYA 540
DB 494 LESLKRTSYIVQYMASTAGCTGNTSINFKTLSPFVFEILLITSLIGGLILLIILTYA 532
QY 541 YGLKPNKLTILCWPVNP 560
DB 533 --EPRSSDKHTHC--PPCPAP 549

RESULT 10
US-10-227-884-92
Sequence 92, Application US/1022784
Publication No. US20030027988A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Collin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C79
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/081955
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PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-08-10
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PRIOR FILING DATE: 1999-02-10

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PRIOR FILING DATE: 1999-08-03
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PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
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PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
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PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.1%; Score 2546; DB 15; Length 582;
Best Local Similarity 98.7%; Pred. No. 2.2e-215;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

1 MMTWALMMLPSLCKFSLSAALPAKRENISCVYYIRKNTLCTWSPCKETSYQYVYKRYA 60
|||||
33 MMTWALMMLPSLCKFSLSAALPAKRENISCVYYIRKNTLCTWSPCKETSYQYVYKRYA 92
|||||
61 FGEKHNDCTNSTSENBRASCFLPRITIPDNTYIEVEAENGDCVISHMTYWRLEMA 120
|||||
93 FGEKHNDCTNSTSENBRASCFLPRITIPDNTYIEVEAENGDCVISHMTYWRLEMA 152
|||||
121 KTEPKIFRVKPVGLGIRKMIQIEWIKPELAPVSSDLKTYLFRFVNSTSMWEVNAKRNK 180
|||||
153 KTEPKIFRVKPVGLGIRKMIQIEWIKPELAPVSSDLKTYLFRFVNSTSMWEVNAKRNK 212
|||||
181 DKNQYNTLTGLOPFVEYIALRCVAKESKFSMDSQEMKMTDEEAPGGLMLRVLPKPAE 240
|||||
213 DKNQYNTLTGLOPFVEYIALRCVAKESKFSMDSQEMKMTDEEAPGGLMLRVLPKPAE 272
|||||
241 ADGRPVRLWKARGADVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGCESPWV 300
|||||

|||||
Db 273 ADGRPRVLLMKAGCAVLEKTLGYNIMYYESNTNLEFMTNTNOQLHLGSEFW 332
QY 301 SMISVNSLKGSPVATLRIPAIORSEFOCIEVQACVADOLVYKNOSSALDVTNMTMEF 360
Db 333 SMISVNSLKGSPVATLRIPAIORSEFOCIEVQACVADOLVYKNOSSALDVTNMTMEF 392
QY 361 PDVDSPTLLSMESVSQATNMTIQODKLKPEWCYNISVYPMHLDRKGEPSIOAYAKGV 420
Db 393 PDVDSPTLLSMESVSQATNMTIQODKLKPEWCYNISVYPMHLDRKGEPSIOAYAKGV 452
QY 421 PSEGETVENIGVTVITITWKEIPKSEKGIICNTTIFYOAGSGKFSKYVNSI 476
Db 453 PSEGETVENIGVTVITITWKEIPKSEKGIICNTTIFYOAGSGKFSKYVNSI 508

RESULT 11
US-10-230-163-92
Sequence 92, Application US/10230163
Publication No. US20030036635A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Maty
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED, AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C96
CURRENT APPLICATION NUMBER: US/10/230,163
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
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;; PRIOR APPLICATION NUMBER: 60/089538
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 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.1%; Score 2546; DB 15; Length 582;
 Best Local Similarity 98.7%; Pred. No. 2,2e-215;
 Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MMWTWALMMLPSLCKFSLALPAKPENISCVYYRRKULCTWSPGKSTYTQYTKRTYA 60
 Db 33 MMWTWALMMLPSLCKFSLALPAKPENISCVYYRRKULCTWSPGKSTYTQYTKRTYA 92
 QY 61 FGEKHNDCTNNSSENKASCSFPLRITTPDNTTIVEAENGNGVYKSHMTYRLENIA 120
 Db 93 FGEKHNDCTNNSSENKASCSFPLRITTPDNTTIVEAENGNGVYKSHMTYRLENIA 152
 QY 121 KTEPPKIFRYKPVGLIRMIQIEIKPELAPVSSDLKYTLRFRTVNSTSMVEVFAKRNK 180
 Db 153 KTEPPKIFRYKPVGLIRMIQIEIKPELAPVSSDLKYTLRFRTVNSTSMVEVFAKRNK 212
 QY 181 DKNOTVNLGTLOPTEVIALRCAYKESKFWSDMSQKMGTEEADPCGLEMLRVLPKPAE 240
 Db 213 DKNOTVNLGTLOPTEVIALRCAYKESKFWSDMSQKMGTEEADPCGLEMLRVLPKPAE 272
 QY 241 ADGRRPVRLLMKKRGAAPVLEKTYGYNIMVYPPESNTNLTETMTNTNOOLEHLGGSFVW 300
 Db 273 ADGRRPVRLLMKKRGAAPVLEKTYGYNIMVYPPESNTNLTETMTNTNOOLEHLGGSFVW 332
 QY 301 SMISYNSLGKSPVTLRIPATQESFOCIEYMQACVAEDOLVYKQSSALDVNTMTIEWF 360
 Db 333 SMISYNSLGKSPVTLRIPATQESFOCIEYMQACVAEDOLVYKQSSALDVNTMTIEWF 392
 QY 361 PDVDEPTLTSWESVSQATMTTIOODKLKPEWCYNISVYPMHLHDVGEPSYQAYAREGV 420
 Db 393 PDVDEPTLTSWESVSQATMTTIOODKLKPEWCYNISVYPMHLHDVGEPSYQAYAREGV 452
 QY 421 PSEGPETKVENIGVKTYYTITMKELPKSEKGIICNTYITFOAEQKGFSTVNSI 476
 Db 453 PSEGPETKVENIGVKTYYTITMKELPKSEKGIICNTYITFOAEQKGFSTVNSI 508

RESULT 12
 US-10-230-338-92
 : Sequence 92, Application US/10230338
 : Publication No. US2003004934A1
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Gerritsen, Mary
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Smith, Victoria
 : APPLICANT: Stephan, Jean-Philippe F.
 : APPLICANT: Watanabe, Colin L.
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P3530P1C92
 : CURRENT APPLICATION NUMBER: US/10/230.338
 : PRIOR FILING DATE: 2002-08-28
 : PRIOR APPLICATION NUMBER: 10/119,480
 : PRIOR FILING DATE: 2002-04-09
 : PRIOR APPLICATION NUMBER: 60/059113
 : PRIOR FILING DATE: 1997-09-17
 : PRIOR APPLICATION NUMBER: 60/062287
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/063549
 : PRIOR FILING DATE: 1997-10-28
 : PRIOR APPLICATION NUMBER: 60/064103
 : PRIOR FILING DATE: 1997-10-31
 : PRIOR APPLICATION NUMBER: 60/069873
 : PRIOR FILING DATE: 1997-12-17
 : PRIOR APPLICATION NUMBER: 60/078910
 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/079294

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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-92

Query Match
Best Local Similarity 98.7%; Score 2546; DB 15; Length 582;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 60
DB 33 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 92
OY 61 FGEKHDNCTTSSSENASCSEFLPRITIPDNTTIEVEAENGCVIKSHMTYRLNIA 120
DB 93 FGEKHDNCTTSSSENASCSEFLPRITIPDNTTIEVEAENGCVIKSHMTYRLNIA 152
OY 121 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMWEVNFARKRK 180
DB 153 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMWEVNFARKRK 212
OY 181 DKNOTYNTGLQPTPEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 240
DB 213 DKNOTYNTGLQPTPEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 272
OY 241 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLCGESFW 300
DB 273 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLCGESFW 332
OY 301 SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 360
DB 333 SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 392
OY 361 PDVNSEPTTSLMESVSQATNMTIOODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
DB 393 PDVNSEPTTSLMESVSQATNMTIOODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 452
OY 421 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGSGKGFKNHSEV 476
DB 453 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGSGKGFKNHSEV 508

RESULT 13
US-10-218-631-92
; Sequence 92, Application US/10218631
; Publication NO. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218.631
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-92

Query Match
Best Local Similarity 98.7%; Score 2546; DB 15; Length 582;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 60
DB 33 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 92
OY 61 FGEKHDNCTTSSSENASCSEFLPRITIPDNTTIEVEAENGCVIKSHMTYRLNIA 120
DB 93 FGEKHDNCTTSSSENASCSEFLPRITIPDNTTIEVEAENGCVIKSHMTYRLNIA 152
OY 121 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMWEVNFARKRK 180
DB 153 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMWEVNFARKRK 212
OY 181 DKNOTYNTGLQPTPEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 240
DB 213 DKNOTYNTGLQPTPEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 272
OY 241 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLCGESFW 300
DB 273 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLCGESFW 332
OY 301 SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 360
DB 333 SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 392
OY 361 PDVNSEPTTSLMESVSQATNMTIOODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
DB 393 PDVNSEPTTSLMESVSQATNMTIOODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 452
OY 421 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGSGKGFKNHSEV 476
DB 453 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGSGKGFKNHSEV 508

RESULT 14
US-10-230-414-92
; Sequence 92, Application US/10230414
; Publication NO. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC98
CURRENT APPLICATION NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 92
LENGTH: 582
TYPE: PRT
ORGANISM: Homo Sapien
US-10-230-414-92

Query Match 65.1%; Score 2546; DB 15; Length 582;
Best Local Similarity 98.7%; Pred. No. 2.2e-215;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAMTWALMLPSLCKFSLAALPAPKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 60
DB 33 MAMTWALMLPSLCKFSLAALPAPKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 92
QY 61 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEANGGVIKSHMTYRLENIA 120
DB 93 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEANGGVIKSHMTYRLENIA 152
QY 121 KTEPPKIFRVKPVGLIKRMIOIEWIKPELAVSSDLKTYLFRFVNSTSMVEVNAKRRK 180
DB 153 KTEPPKIFRVKPVGLIKRMIOIEWIKPELAVSSDLKTYLFRFVNSTSMVEVNAKRRK 212
QY 181 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAPGGLMLRVLPKPAE 240
DB 213 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAPGGLMLRVLPKPAE 272
QY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGSESPV 300
DB 273 ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGSESPV 332
QY 301 SMIVNSLGSKSPVATLRIPALIOESFOCIEYMOACVADOLVVKWSSALDVNTMTWME 360
DB 333 SMIVNSLGSKSPVATLRIPALIOESFOCIEYMOACVADOLVVKWSSALDVNTMTWME 392
QY 361 PDVSEPTLTSWESVSQATNWTIOODKLKPFWCYNISVYPMHLHDKVGEPSYIOAYAKGV 420
DB 393 PDVSEPTLTSWESVSQATNWTIOODKLKPFWCYNISVYPMHLHDKVGEPSYIOAYAKGV 452
QY 421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNYTIFYOAEKGKGFCKHANHSEV 508
PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNYTIFYOAEKGKGFCKHANHSEV 508

DB 453 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNYTIFYOAEKGKGFCKHANHSEV 508
RESULT 15
US-10-216-159A-92
Sequence 92, Application US/10216159A
Publication No. US20030069397A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC6
CURRENT APPLICATION NUMBER: US/10/216,159A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 92
LENGTH: 582
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-159A-92

Query Match 65.1%; Score 2546; DB 15; Length 582;
Best Local Similarity 98.7%; Pred. No. 2.2e-215;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAMTWALMLPSLCKFSLAALPAPKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 60
DB 33 MAMTWALMLPSLCKFSLAALPAPKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 92
QY 61 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEANGGVIKSHMTYRLENIA 120
DB 93 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEANGGVIKSHMTYRLENIA 152
QY 121 KTEPPKIFRVKPVGLIKRMIOIEWIKPELAVSSDLKTYLFRFVNSTSMVEVNAKRRK 180
DB 153 KTEPPKIFRVKPVGLIKRMIOIEWIKPELAVSSDLKTYLFRFVNSTSMVEVNAKRRK 212
QY 181 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAPGGLMLRVLPKPAE 240
DB 213 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAPGGLMLRVLPKPAE 272
QY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGSESPV 300

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Db 273 ADGRRPVRLLMKKARGAVLEKTLGYNTMYYPESNTNLTETMNTNNOOLELHIGSEFW 332
OY 301 SMISYNSLGKSPVATLRIPAIQKSFQCI EYMOACVAEDOLVVKWQSSALDVNTWMIEMF 360
Db 333 SMISYNSLGKSPVATLRIPAIQKSFQCI EYMOACVAEDOLVVKWQSSALDVNTWMIEMF 392
OY 361 PDVDEPTTLSMESYSQATNMTIOODKLPFCYNISSVYPM LHDKVGEPSIOAYAKEGV 420
Db 393 PDVDEPTTLSMESYSQATNMTIOODKLPFCYNISSVYPM LHDKVGEPSIOAYAKEGV 452
OY 421 PSEGPETKVENIGVKTVTITWKELPKSERKGIICNYTIFYOAGGKGFSTVNSSI 476
Db 453 PSEGPETKVENIGVKTVTITWKELPKSERKGIICNYTIFYOAGGKGFCKHAHSEV 508
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Search completed: August 4, 2003, 11:21:07
Job time : 30 secs

PI Maurer MF:
 XX WPI: 2002-090519/12.
 DR N-PSDB: ABA93767.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX
 PS Claim 18: Page 166-168; 235pp: English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 732 AA:
 Query Match 100.0%; Score 3908; DB 23; Length 732;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMTWALMLPSCFKSLAALPAKPNISCVYYRRKNLCTWSPGKETSQYTVKRTYA 60
 DB 1 MMTWALMLPSCFKSLAALPAKPNISCVYYRRKNLCTWSPGKETSQYTVKRTYA 60
 QY 61 FGEKHNDCTNSTSENASCSEFFLPRTIPDNYTTEVAENDGVYKSHMTYWRLENIA 120
 DB 61 FGEKHNDCTNSTSENASCSEFFLPRTIPDNYTTEVAENDGVYKSHMTYWRLENIA 120
 QY 121 KTEPPRIEFVKPYLGKRIQIEMIKBELAPVSSDLKYLRLRRTVNSTSMVEYNFAKNRK 180
 DB 121 KTEPPRIEFVKPYLGKRIQIEMIKBELAPVSSDLKYLRLRRTVNSTSMVEYNFAKNRK 180
 QY 121 KTEPPRIEFVKPYLGKRIQIEMIKBELAPVSSDLKYLRLRRTVNSTSMVEYNFAKNRK 180
 DB 121 KTEPPRIEFVKPYLGKRIQIEMIKBELAPVSSDLKYLRLRRTVNSTSMVEYNFAKNRK 180
 QY 181 DKNQYNTLGTLPFTFEYVALRCAYKESKESFMSDQEKKGMTBEERPCLELMRYLKAPE 240
 DB 181 DKNQYNTLGTLPFTFEYVALRCAYKESKESFMSDQEKKGMTBEERPCLELMRYLKAPE 240
 QY 181 DKNQYNTLGTLPFTFEYVALRCAYKESKESFMSDQEKKGMTBEERPCLELMRYLKAPE 240
 DB 181 DKNQYNTLGTLPFTFEYVALRCAYKESKESFMSDQEKKGMTBEERPCLELMRYLKAPE 240
 QY 241 ADGRRRPVRLMKKARGAPVLEKTLGYNLWYVESNTNLETNNTNNOOLEHLGGESEFVY 300
 DB 241 ADGRRRPVRLMKKARGAPVLEKTLGYNLWYVESNTNLETNNTNNOOLEHLGGESEFVY 300
 QY 301 SMISYNSLGSKSPVALRLRPAIDOKSFQCIENVMOACVAEDOLVVKQSSALDVNTWMIEMF 360
 DB 301 SMISYNSLGSKSPVALRLRPAIDOKSFQCIENVMOACVAEDOLVVKQSSALDVNTWMIEMF 360
 QY 301 SMISYNSLGSKSPVALRLRPAIDOKSFQCIENVMOACVAEDOLVVKQSSALDVNTWMIEMF 360
 DB 301 SMISYNSLGSKSPVALRLRPAIDOKSFQCIENVMOACVAEDOLVVKQSSALDVNTWMIEMF 360
 QY 361 PDVDEPPTLSWESVSQATNMTIQQDKLKPFCVNIISVYPMIHDVGEPSYIOAYAKAGV 420
 DB 361 PDVDEPPTLSWESVSQATNMTIQQDKLKPFCVNIISVYPMIHDVGEPSYIOAYAKAGV 420
 QY 421 PSEGETVENIGVATVTITWKEIPKSERKGIICVYTFYQAEKSGSKYVNSSILOYG 480
 DB 421 PSEGETVENIGVATVTITWKEIPKSERKGIICVYTFYQAEKSGSKYVNSSILOYG 480
 QY 481 LESLAKRSTSYVOVMASTSAAGTNGTSINFKTLSFVSVEIILITSLIGGLILITLVA 540
 DB 481 LESLAKRSTSYVOVMASTSAAGTNGTSINFKTLSFVSVEIILITSLIGGLILITLVA 540
 QY 541 YGLKKPNKLTHLCPYVNPAPASSIATYHGDGDKDLNLAKESDVSNTEDRIILKPCSPS 600
 DB 541 YGLKKPNKLTHLCPYVNPAPASSIATYHGDGDKDLNLAKESDVSNTEDRIILKPCSPS 600

QY 601 DKLVIDLVNFGVNLQEIETDEARTGOENNKGKNGYVCPFRPDCPLGKSFEEPLVS 660
 DB 601 DKLVIDLVNFGVNLQEIETDEARTGOENNKGKNGYVCPFRPDCPLGKSFEEPLVS 660
 QY 661 PEIPRRKSQYLRSMFPGSTREAKEQLLFSQSGLVPDHLCEGAPNLYLNSTYAREFLV 720
 DB 661 PEIPRRKSQYLRSMFPGSTREAKEQLLFSQSGLVPDHLCEGAPNLYLNSTYAREFLV 720
 QY 721 SEKLPEHTKGEV 732
 DB 721 SEKLPEHTKGEV 732
 RESULT 2
 ID ABB54364
 XX ABB54364 standard; Protein: 764 AA.
 AC ABB54364:
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human NR10.4 splicing variant protein SEQ ID NO:4.
 XX
 KW NR10: splicing variant; haematopoietin receptor; immunomodulator;
 KW haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation.
 OS Homo sapiens.
 XX
 PN WO200277230-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 22-MAR-2002; 2002WO-JP02769.
 XX
 PR 26-MAR-2001; 2001JP-0087298.
 XX
 PA (CHUS) CHUGAI SETYAKU KK.
 XX
 PI Maeda M, Yaguchi N, Hasegawa M;
 XX
 DR WPI: 2003-018925/01.
 XX
 DR N-PSDB: ABB083364.
 XX
 PT NR10 splicing variants of hematopoietin receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases.
 PS Claim 1: Fig 6: 250pp: Japanese.
 XX
 XX The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietin receptor genes participate
 CC in vivo immunomodulation and haematopoietic cell regulation, and in
 CC the search for haematopoietic factors capable of functionally binding
 CC to the receptors. The present sequence represents the human NR10.4
 CC protein from the present invention.
 CC
 XX
 SQ Sequence 764 AA:
 Query Match 100.0%; Score 3908; DB 24; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMTWALMLPSCFKSLAALPAKPNISCVYYRRKNLCTWSPGKETSQYTVKRTYA 60
 DB 33 MMTWALMLPSCFKSLAALPAKPNISCVYYRRKNLCTWSPGKETSQYTVKRTYA 92
 QY 61 FGEKHNDCTNSTSENASCSEFFLPRTIPDNYTTEVAENDGVYKSHMTYWRLENIA 120

Db 93 GGEKNDCTNTSSSENASCSPFLPRITPDNTTIEVEANGGVIRKSHMTYRLENIA 152
 QY 121 KTEPKIFRVPVIGIKRMIOIEWIKPELAPVSSDLKTYLTFRTVNSTSMWEVFAKNRK 180
 Db 153 KTEPKIFRVPVIGIKRMIOIEWIKPELAPVSSDLKTYLTFRTVNSTSMWEVFAKNRK 212
 QY 181 DKNOTYNTLGTQPTFEYVIALRCVAKESKFWDSQEMKMGTEEBAPCGLELMVLRPAE 240
 Db 213 DKNOTYNTLGTQPTFEYVIALRCVAKESKFWDSQEMKMGTEEBAPCGLELMVLRPAE 272
 QY 241 ADGRPPVRLMKKARGAVLEKTLGYNIMWY PESTNTLTETMTNTNOOLEHLGSEFW 300
 Db 273 ADGRPPVRLMKKARGAVLEKTLGYNIMWY PESTNTLTETMTNTNOOLEHLGSEFW 332
 QY 301 SMISYNSLGSPVATLRIPATQKSFQCI EVMQACVAEDQLVVKWQSSALDVNTMTIEMF 360
 Db 333 SMISYNSLGSPVATLRIPATQKSFQCI EVMQACVAEDQLVVKWQSSALDVNTMTIEMF 392
 QY 361 PDVDEPTTLTSMESVSQATNTTIOODKLRPWCYNISVYPMJHDKVGPYSIOAYAKGV 420
 Db 393 PDVDEPTTLTSMESVSQATNTTIOODKLRPWCYNISVYPMJHDKVGPYSIOAYAKGV 452
 QY 421 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSSILOYG 480
 Db 453 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSSILOYG 512
 QY 481 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVVEILLITSLIGGLILLITLVA 540
 Db 513 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVVEILLITSLIGGLILLITLVA 572
 QY 541 YGLKPKPKLTHLCMPTVPNPAESSIATWHDGDFKDKLNLKESDSDVNTEDRILKPCSTPS 600
 Db 573 YGLKPKPKLTHLCMPTVPNPAESSIATWHDGDFKDKLNLKESDSDVNTEDRILKPCSTPS 632
 QY 601 DKLVYDKLVNFGVNLQEIFTDEARTGOENNLGGEKNKYVTCPPRPDCLPKSFEELPVS 660
 Db 633 DKLVYDKLVNFGVNLQEIFTDEARTGOENNLGGEKNKYVTCPPRPDCLPKSFEELPVS 692
 QY 661 PEIPPRKSOYLRSRMPECTREPAKEQLLFSGOSLVPDHLCEGAPNPLKNSVAREFLV 720
 Db 693 PEIPPRKSOYLRSRMPECTREPAKEQLLFSGOSLVPDHLCEGAPNPLKNSVAREFLV 752
 QY 721 SEKLPEHTKGEV 732
 Db 753 SEKLPEHTKGEV 764

RESULT 3
 ABP54365
 ID ABP54365 standard; Protein: 764 AA.

XX AC ABP54365;
 XX DT 20-JAN-2003 (first entry)
 XX DE Human NR10.4 splicing variant protein SEQ ID NO:6.
 XX DE NR10.4 splicing variant; haematopoietin receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation.
 XX OS Homo sapiens.
 XX PN WO200277230-A1.
 XX PD 03-OCT-2002.
 XX PF 22-MAR-2002; 2002WO-JP02769.
 XX PR 26-MAR-2001; 2001JP-0087298.
 XX PA (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;
 XX WP1: 2003-018925/01.
 DR N-PSDB; ABQ83365.
 XX NR10 splicing variants of haematopoietin receptor proteins and encoded
 PT genes, applicable in searching haematopoietic factors and developing
 PT remedies for immunological and haematopoietic diseases
 PS Claim 1; Fig 7-9; 250pp: Japanese.
 XX The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietin receptor genes participate
 CC in vivo immunomodulation and haematopoietic cell regulation, and in
 CC the search for haematopoietic factors capable of functionally binding
 CC to the receptors. The present sequence represents the human NR10.4
 CC protein from the present invention.
 SO Sequence 764 AA:
 Query Match 100.0%; Score 3908; DB 24; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWTALMLPDLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYQYVTKRYA 60
 Db 33 MMWTALMLPDLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYQYVTKRYA 92
 QY 61 GGEKNDCTNTSSSENASCSPFLPRITPDNTTIEVEANGGVIRKSHMTYRLENIA 120
 Db 93 GGEKNDCTNTSSSENASCSPFLPRITPDNTTIEVEANGGVIRKSHMTYRLENIA 152
 QY 121 KTEPKIFRVPVIGIKRMIOIEWIKPELAPVSSDLKTYLTFRTVNSTSMWEVFAKNRK 180
 Db 153 KTEPKIFRVPVIGIKRMIOIEWIKPELAPVSSDLKTYLTFRTVNSTSMWEVFAKNRK 212
 QY 181 DKNOTYNTLGTQPTFEYVIALRCVAKESKFWDSQEMKMGTEEBAPCGLELMVLRPAE 240
 Db 213 DKNOTYNTLGTQPTFEYVIALRCVAKESKFWDSQEMKMGTEEBAPCGLELMVLRPAE 272
 QY 241 ADGRPPVRLMKKARGAVLEKTLGYNIMWY PESTNTLTETMTNTNOOLEHLGSEFW 300
 Db 273 ADGRPPVRLMKKARGAVLEKTLGYNIMWY PESTNTLTETMTNTNOOLEHLGSEFW 332
 QY 301 SMISYNSLGSPVATLRIPATQKSFQCI EVMQACVAEDQLVVKWQSSALDVNTMTIEMF 360
 Db 333 SMISYNSLGSPVATLRIPATQKSFQCI EVMQACVAEDQLVVKWQSSALDVNTMTIEMF 392
 QY 361 PDVDEPTTLTSMESVSQATNTTIOODKLRPWCYNISVYPMJHDKVGPYSIOAYAKGV 420
 Db 393 PDVDEPTTLTSMESVSQATNTTIOODKLRPWCYNISVYPMJHDKVGPYSIOAYAKGV 452
 QY 421 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSSILOYG 480
 Db 453 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTFYQAEKGKFSKTVNSSILOYG 512
 QY 481 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVVEILLITSLIGGLILLITLVA 540
 Db 513 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVVEILLITSLIGGLILLITLVA 572
 QY 541 YGLKPKPKLTHLCMPTVPNPAESSIATWHDGDFKDKLNLKESDSDVNTEDRILKPCSTPS 600
 Db 573 YGLKPKPKLTHLCMPTVPNPAESSIATWHDGDFKDKLNLKESDSDVNTEDRILKPCSTPS 632
 QY 601 DKLVYDKLVNFGVNLQEIFTDEARTGOENNLGGEKNKYVTCPPRPDCLPKSFEELPVS 660
 Db 633 DKLVYDKLVNFGVNLQEIFTDEARTGOENNLGGEKNKYVTCPPRPDCLPKSFEELPVS 692
 QY 661 PEIPPRKSOYLRSRMPECTREPAKEQLLFSGOSLVPDHLCEGAPNPLKNSVAREFLV 720

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DB      693 PEIPRKSQYLNRSMPEGSTREPAKEDQLSGSLVPHDLCEGAPNPYLKNSVTAREFLV 752
OY      721 SEKLPEHTKGEV 732
        |||||
DB      753 SEKLPEHTKGEV 764

RESULT 4
AAE24024
ID      AAE24024 standard: Protein: 745 AA.
XX      AAE24024;
AC      AAE24024;
DT      23-SEP-2002 (first entry)
XX      Human haematopoietin receptor 1 (HPRI) protein.
DE      Human haematopoietin receptor 1 (HPRI) protein.
XX      Human; haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;
KM      pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
KM      neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
KM      cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KM      ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
KM      osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;
KM      anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
KM      demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
KM      vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KM      stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
KM      ischaemic disease.
XX      Homo sapiens.
XX      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      20..32
FT      /Label= Signal_peptide
FT      33..745
FT      /note= "Human mature HPRI protein"
FT      33..241
FT      /note= "Cytokine receptor domain"
FT      83
FT      /note= "This residue changes to Ala during
FT      allelic variation"
FT      135..138
FT      /note= "Proline-rich linker"
FT      139..241
FT      /note= "C-terminal cytokine receptor subdomain"
FT      168
FT      /note= "This residue changes to Asn during
FT      allelic variation"
FT      187
FT      /note= "This residue changes to Thr during
FT      allelic variation"
FT      224..228
FT      /note= "MSXMS motif"
FT      242..515
FT      /note= "Fibronectin repeat"
FT      361
FT      /note= "This residue changes to Pro during
FT      allelic variation"
FT      362
FT      /note= "This residue changes to Gly during
FT      allelic variation"
FT      510
FT      /note= "This residue changes to Asn during
FT      allelic variation"
FT      517
FT      /note= "Encoded by GAC; This residue changes to
FT      Asp during allelic variation"
FT      526..556
FT      /note= "Extended transmembrane domain"
FT      533..552
FT      /note= "Core transmembrane domain"
FT      553..745
FT      /note= "Cytoplasmic domain"

```

```

FT      Domain
FT      563..573
FT      /note= "Box1 conserved motif"
FT      588..592
FT      /note= "Repeat peptide"
FT      597..601
FT      /note= "Repeat peptide"
FT      603..607
FT      /note= "Repeat peptide"
FT      614..618
FT      /note= "Repeat peptide"
FT      619..623
FT      /note= "Repeat peptide"
FT      631..641
FT      /note= "Repeat peptide"
FT      631..641
FT      /note= "Box2 conserved motif"
FT      635..639
FT      /note= "Repeat peptide"
FT      679
FT      /note= "This residue changes to Gly during
FT      allelic variation"

WO200229060-A2.
11-APR-2002.
05-OCT-2001; 2001WO-US31634.
06-OCT-2000; 2000US-238706P.
13-OCT-2000; 2000US-240476P.
20-FEB-2001; 2001US-270282P.
(IMMV ) IMMUNEX CORP.
Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
WPT: 2002-330172/36.
N-PSDB; AAD38772.

Human and murine haematopoietin receptor polypeptides HPRI and HPR2,
useful for treating cell proliferation, metabolic, and reproductive
hormone related conditions -
Claim 1; Page 84-87; 136pp; English.

The present invention relates to human and murine haematopoietin receptor
polypeptides HPRI and HPR2. Sequences of the invention are useful for
treating cell proliferation conditions e.g., pancytopenia, leukopenia,
anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
resulting from a lack of bone-forming cells. They are also useful for
treating cell proliferation conditions such as leukaemia and tumour
metastasis, osteoporosis resulting from an excess of bone-resorbing
cells. HPR sequences are also useful for treating medical conditions and
diseases such as cell proliferation, metabolic and reproductive hormone
related conditions. They are useful for treating various haematologic and
oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
squamous cell carcinoma), haematologic disorders, anemias (e.g., anaemia
of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
dysplastic syndromes (including refractory anaemia, refractory anaemia
with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
myeloid metaplasia, osteoclast disorders that lead to bone loss such
as osteoporosis including post-menopausal osteoporosis, peridontitis
resulting in tooth loosening or loss, prosthesis loosening after joint
replacement, neurodegenerative conditions (e.g., acute polynuropathy,
Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
myasthenia gravis, chronic neuronal degeneration, stroke including
cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
for treating various other disorders such as osteoporosis, obesity.

```

CC deficient mammary development and infertility. The present sequence
is human HPR1 protein.

XX Sequence 745 AA;

Query Match 99.7%; Score 3896; DB 23; Length 745;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 1 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLCTWVGKETSITYQYVKKRYA 60
DB 14 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLCTWVGKETSITYQYVKKRYA 73
OY 61 FGEKHDNCTNNTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 120
DB 74 FGEKHDNCTNNTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 133
OY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMVEVFAKRRK 180
DB 134 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMVEVFAKRRK 193
OY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQSKMGTEEBAPCGLELMRYLKPAAE 240
DB 194 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQSKMGTEEBAPCGLELMRYLKPAAE 253
OY 241 ADGRRPVLLMKKARGAPVLEKTLGYNIWYYPESNTNLTEMTNTNOLHLGSEFVW 300
DB 254 ADGRRPVLLMKKARGAPVLEKTLGYNIWYYPESNTNLTEMTNTNOLHLGSEFVW 313
OY 301 SMISYNSLGKSPVATLIRPAIQEKSFQCIEMVQACVADOLVYKMOSSALDVTMTMEWF 360
DB 314 SMISYNSLGKSPVATLIRPAIQEKSFQCIEMVQACVADOLVYKMOSSALDVTMTMEWF 373
OY 361 PDVNSEPTLSMESVSQATMTWTIOODKLKPCWCYNISVYPLHDKVGEPSIOAYAREGV 420
DB 374 PDVNSEPTLSMESVSQATMTWTIOODKLKPCWCYNISVYPLHDKVGEPSIOAYAREGV 433
OY 421 PSEGPETKVENIGKVTITWKEIPKSEKGIICNTITFYQAEKGKFSKTVNSIIQYG 480
DB 434 PSEGPETKVENIGKVTITWKEIPKSEKGIICNTITFYQAEKGKFSKTVNSIIQYG 493
OY 481 LESLKRTSYIVQVMASTAGGTNGTSINFKTISFVEIILITSLIGGILLIILITVA 540
DB 494 LESLKRTSYIVQVMASTAGGTNGTSINFKTISFVEIILITSLIGGILLIILITVA 553
OY 541 YGLKKPKKTLHLCPYTPNPAESSIATWBGDDFKDLNLEKSDSVNTEEDILKPCSTPS 600
DB 554 YGLKKPKKTLHLCPYTPNPAESSIATWBGDDFKDLNLEKSDSVNTEEDILKPCSTPS 613
OY 601 DKLVLDLVNFGVNLQEIFTEARTGOENNLGGEKNGYVTCPPRPOCPGLKSPFEEELPV 660
DB 614 DKLVLDLVNFGVNLQEIFTEARTGOENNLGGEKNGYVTCPPRPOCPGLKSPFEEELPV 673
OY 661 PEIPPKRSQYLRSMEPEGTREPEAKEQLLFSGOSLVPHLCBEGANPYLKNSTVAREFLV 720
DB 674 PEIPPKRSQYLRSMEPEGTREPEAKEQLLFSGOSLVPHLCBEGANPYLKNSTVAREFLV 733
OY 721 SEKLPEHTKGEV 732
DB 734 SEKLPEHTKGEV 745

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RESULT 5

ABB05738 standard; Protein: 649 AA.

ABB05738;

01-MAY-2002 (first entry)

Human zcytor17 protein sequence SEQ ID NO:46.

zcytor17: chromosome 5; 5q11: cytokine receptor; immunomodulatory;

KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

XX WO200200721-A2.

XX 03-JAN-2002.

XX 26-JUN-2001; 2001WO-US20484.

XX 26-JUN-2000; 2000US-214282P.

XX 26-JUN-2000; 2000US-214955P.

XX 08-FEB-2001; 2001US-267963P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuiper JJ;

XX Maurer ME;

XX WPI; 2002-090519/12.

XX N-PSDB; ABA93803.

XX Claim 18: Page 195-197; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17. zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention.

XX Sequence 649 AA;

Query Match 87.1%; Score 3405.5; DB 23; Length 649;

Best Local Similarity 99.1%; Pred. No. 81e-280;

Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

```

OY 1 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLCTWVGKETSITYQYVKKRYA 60
DB 1 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLCTWVGKETSITYQYVKKRYA 60
OY 61 FGEKHDNCTNNTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 120
DB 61 FGEKHDNCTNNTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 120
OY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMVEVFAKRRK 180
DB 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMVEVFAKRRK 180
OY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQSKMGTEEBAPCGLELMRYLKPAAE 240
DB 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQSKMGTEEBAPCGLELMRYLKPAAE 240
OY 241 ADGRRPVLLMKKARGAPVLEKTLGYNIWYYPESNTNLTEMTNTNOLHLGSEFVW 300
DB 241 ADGRRPVLLMKKARGAPVLEKTLGYNIWYYPESNTNLTEMTNTNOLHLGSEFVW 300

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Db 241 ADGRPRVRLMKKARGAVLEKTLGYNIWYYPESNTLTETMNTTNOOLELHLGSEFMV 300
 QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCI EWQACVAEDQLVKQSSALDVNTMIMWF 360
 Db 301 SMISYNSLGKSPVATLRIPAIQEKSFQCI EWQACVAEDQLVKQSSALDVNTMIMWF 360
 QY 361 PDVDEPTTLTSMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
 Db 361 PDVDEPTTLTSMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
 QY 421 PSEGETVENIGVKTVTITTKETPKSERKGIICNTTTFYAEGKGSKTVNSSIIQYG 480
 Db 421 PSEGETVENIGVKTVTITTKETPKSERKGIICNTTTFYAEGKGSKTVNSSIIQYG 480
 QY 481 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFVEIILITSLIGGLIILITLVA 540
 Db 481 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFVEIILITSLIGGLIILITLVA 540
 QY 541 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
 Db 541 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
 QY 601 DKLVYDKLVNFGNVLOEIFTDEARTGQENNLGGEKNG---YVTCF 643
 Db 601 DKLVYDKLVNFGNVLOEIFTDEARTGQENNLGGEKNGTRILSSCP 646
 Db
 RESULT 6
 AAB51244
 ID AAB51244 standard; Protein: 662 AA.
 AC AAB51244;
 XX 26-MAR-2001 (first entry)
 DT
 DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.
 XX
 KM Human: haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
 KM immunoregulation; haematopoietic cell regulation; transmembrane;
 KM immune disorder; haematopoietic disorder; autoimmune disease; allergy;
 KM metal allergy; pollen allergy.
 XX
 OS Homo sapiens.
 OS
 PN WO200075314-A1.
 PD 14-DEC-2000.
 PE 01-JUN-2000; 2000WO-JP03556.
 PF
 PR 02-JUN-1999; 99JP-0155797.
 PR 30-JUL-1999; 99JP-0217797.
 XX
 PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PL Maeda M, Yaguchi N;
 DR WPI: 2001-061720/07.
 DR N-PSDB: AAC92350.
 XX
 PT Hematopoietin receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PT diseases and allergies
 XX
 PS Claim 1: Fig 13-14; 127pp; Japanese.
 XX
 CC The present sequence represents a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell
 CC regulation in vivo, and is useful in searching for haematopoietic
 CC factors capable of binding to the receptor. NR10 can be used for the
 CC identification of substances for the treatment and prevention of immune

CC and haematopoietic disorders including autoimmune diseases and allergies
 CC such as metal and pollen allergy.
 XX
 SO Sequence 662 AA:
 QY 1 MMNTWALMLPSLCKFSLAALPARKENISCYYYRKNLTCTWSPEKETSYYQYVKKRYA 60
 Db 14 MMNTWALMLPSLCKFSLAALPARKENISCYYYRKNLTCTWSPEKETSYYQYVKKRYA 73
 QY 61 FGEKHNDCTNSTSENKASCFELPRITPDNTIEVEANGDVISHSMTYMLNENIA 120
 Db 74 FGEKHNDCTNSTSENKASCFELPRITPDNTIEVEANGDVISHSMTYMLNENIA 133
 QY 121 KTEPPKIFRVRPVLGIRKRIQIEWIKPELAVSSDLKYTLRFRVNSTSMMEVFAKNRK 180
 Db 134 KTEPPKIFRVRPVLGIRKRIQIEWIKPELAVSSDLKYTLRFRVNSTSMMEVFAKNRK 193
 QY 181 DKNQTYNLTGLQPTFEYVIALRCAYKESKESFMSDSQEMGNTBEAPCGLELMRYLAKAE 240
 Db 194 DKNQTYNLTGLQPTFEYVIALRCAYKESKESFMSDSQEMGNTBEAPCGLELMRYLAKAE 253
 QY 241 ADGRPRVRLMKKARGAVLEKTLGYNIWYYPESNTLTETMNTTNOOLELHLGSEFMV 300
 Db 254 ADGRPRVRLMKKARGAVLEKTLGYNIWYYPESNTLTETMNTTNOOLELHLGSEFMV 313
 QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCI EWQACVAEDQLVKQSSALDVNTMIMWF 360
 Db 314 SMISYNSLGKSPVATLRIPAIQEKSFQCI EWQACVAEDQLVKQSSALDVNTMIMWF 373
 QY 361 PDVDEPTTLTSMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
 Db 374 PDVDEPTTLTSMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 433
 QY 421 PSEGETVENIGVKTVTITTKETPKSERKGIICNTTTFYAEGKGSKTVNSSIIQYG 480
 Db 434 PSEGETVENIGVKTVTITTKETPKSERKGIICNTTTFYAEGKGSKTVNSSIIQYG 493
 QY 481 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFVEIILITSLIGGLIILITLVA 540
 Db 494 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFVEIILITSLIGGLIILITLVA 553
 QY 541 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
 Db 554 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 613
 QY 601 DKLVYDKLVNFGNVLOEIFTDEARTGQENNLGGEKNG---YVTCF 643
 Db 614 DKLVYDKLVNFGNVLOEIFTDEARTGQENNLGGEKNGTRILSSCP 659
 Db
 RESULT 7
 AAE24029
 ID AAE24029 standard; Protein: 662 AA.
 AC AAE24029;
 XX 23-SEP-2002 (first entry)
 DT
 DE Human HPR1 variant protein #3.
 XX
 KM Human: haematopoietin receptor; HPR1; HPR2; cell proliferation;
 KM pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 KM cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KM osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
 KM anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KM demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;

KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KW ischaemic disease; variant.
 XX Homo sapiens.
 OS
 PN W0200229060-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001MO-US31634.
 XX
 PR 06-OCT-2000; 2000US-2238706P.
 PR 13-OCT-2000; 2000US-240476P.
 PR 20-FEB-2001; 2001US-270282P.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 DR WPI: 2002-330172/36.
 XX
 PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions -
 XX
 PS Disclosure: Page 112-115; 136pp; English.

CC The present invention relates to human and murine hematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukaemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various haematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC amyotrophic lateral sclerosis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence
 CC is human HPR1 variant protein.
 CC
 XX
 SQ Sequence 662 AA;

Query Match 87.1%; Score 3405.5; DB 23; Length 662;
 Best Local Similarity 99.1%; Pred. No. 8.3e-260;
 Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 MMTWTALMLPSLCFSLALPAKPNISCVYYRKNLTCTWSPGKETSQYVKKRYA 60
 DB 14 MMTWTALMLPSLCFSLALPAKPNISCVYYRKNLTCTWSPGKETSQYVKKRYA 73
 QY 61 FGEKHNDCTNNSSTENRASCFFLPRTITPDNTTIEVEANGDGVKSHMTYRLNIA 120
 DB 74 FGEKHNDCTNNSSTENRASCFFLPRTITPDNTTIEVEANGDGVKSHMTYRLNIA 133

QY 121 KTEPPKIEFRVYPVIGIKRMIOEMIKPELPAPVSSDLKYTLRFRFVNSTSMWEVFAKNRK 180
 DB 134 KTEPPKIEFRVYPVIGIKRMIOEMIKPELPAPVSSDLKYTLRFRFVNSTSMWEVFAKNRK 193
 QY 181 DKNOTYNLGLQPFTEVEVALRCVAVKESKFWSDMSQEKMGMTDEAPCGLELVRVLPAP 240
 DB 194 DKNOTYNLGLQPFTEVEVALRCVAVKESKFWSDMSQEKMGMTDEAPCGLELVRVLPAP 253
 QY 241 ADGRPRVRLMKARCAPVEKTLGNINWYPPSSNTNLETMTNTTNOQLEHLGGSFVW 300
 DB 254 ADGRPRVRLMKARCAPVEKTLGNINWYPPSSNTNLETMTNTTNOQLEHLGGSFVW 313
 QY 301 SMISYNSLGKSPATLIRIPAIQKSFQICFVMAQVADQDLYVKMOSALDVTMTMEWF 360
 DB 314 SMISYNSLGKSPATLIRIPAIQKSFQICFVMAQVADQDLYVKMOSALDVTMTMEWF 373
 QY 361 PDVDSPTLTSWESVSQATNMTIOODKLKPPWCYNISVYEMLDHKVGEPSIOAYAKEGV 420
 DB 374 PDVDSPTLTSWESVSQATNMTIOODKLKPPWCYNISVYEMLDHKVGEPSIOAYAKEGV 433
 QY 421 PSEGPETKVENIGVYTTITWKEIPKSEKGIICNTTIFQVAGGKFSVTWSSIIQYG 480
 DB 434 PSEGPETKVENIGVYTTITWKEIPKSEKGIICNTTIFQVAGGKFSVTWSSIIQYG 493
 QY 481 LESLKRKTSYIVOVMASTSGAGTNGTSINFKTISFVFEILITSLIGGGLITLITVA 540
 DB 494 LESLKRKTSYIVOVMASTSGAGTNGTSINFKTISFVFEILITSLIGGGLITLITVA 553
 QY 541 YGLKPKPKLTHLCPVTPNPFAESSIATWHDDEKDKLNEKSDSVNTEDRILKPCSTPS 600
 DB 554 YGLKPKPKLTHLCPVTPNPFAESSIATWHDDEKDKLNEKSDSVNTEDRILKPCSTPS 613
 QY 601 DKLYIDKLVNFGVNLQEIFTDEARTQGENNIGCKNG---YVTCF 643
 DB 614 DKLYIDKLVNFGVNLQEIFTDEARTQGENNIGCKNGTRLSSCP 659

RESULT 8
 ID ABB05741 standard; Protein: 662 AA.
 AC ABB05741;
 XX
 DF 01-MAY-2002 (first entry)
 DE Human zcytor17 protein sequence SEQ ID NO:54.
 KW zcytor17: chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 OS Homo sapiens.
 XX
 PN W0200200721-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001MO-US20484.
 XX
 PR 26-JUN-2000; 2000US-214282P.
 PR 29-JUN-2000; 2000US-214955P.
 PR 08-FEB-2001; 2001US-267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
 PI Maurer MF;
 DR WPI: 2002-090519/12.

DR N-PSDB: ABA93808.
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders -
 XX
 XX Example 1: Page 204-206; 235pp; English.
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antirhectic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.
 CC
 XX Sequence 662 AA:
 SO
 Query Match 87.1%; Score 3405.5; DB 23; Length 662;
 Best Local Similarity 99.1%; Pred. No. 8.3e-280;
 Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
 QY 1 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKSTYQTVKRTYA 60
 DB 14 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKSTYQTVKRTYA 73
 QY 61 FGEHNDCTNNTSSSENKASCSFLLPRTTIPDNTTIEVEANGGVKSHMTYRLNIA 120
 DB 74 FGEHNDCTNNTSSSENKASCSFLLPRTTIPDNTTIEVEANGGVKSHMTYRLNIA 133
 QY 121 KTEPPKIFRVKPVLGIRMIQIEWIKPELAPVSSDLKTYTLRFVNSTSMWEVFAKNRK 180
 DB 134 KTEPPKIFRVKPVLGIRMIQIEWIKPELAPVSSDLKTYTLRFVNSTSMWEVFAKNRK 193
 QY 181 DKNOTYNTLGLQPTFEYVIALRCVAKESKFSWDSOEKMGTEEPACGLELMRVLPAAE 240
 DB 194 DKNOTYNTLGLQPTFEYVIALRCVAKESKFSWDSOEKMGTEEPACGLELMRVLPAAE 253
 QY 241 ADGRRPRLIMKKARGAPVLEKTLGYNIWYPSNTNLTETMTNTNOOLELHLCGESFW 300
 DB 254 ADGRRPRLIMKKARGAPVLEKTLGYNIWYPSNTNLTETMTNTNOOLELHLCGESFW 313
 QY 301 SMISYNSIGKSPVATLRIPAIOEKSPFQIEVMAQVADOLVVMKQSSALDVNTMIMEF 360
 DB 314 SMISYNSIGKSPVATLRIPAIOEKSPFQIEVMAQVADOLVVMKQSSALDVNTMIMEF 373
 QY 361 PDVDSPTTISWESVSQATMNTIQODKLKPFWCYNISVYPMHLHDVKEPYSIQAYAREGV 420
 DB 374 PDVDSPTTISWESVSQATMNTIQODKLKPFWCYNISVYPMHLHDVKEPYSIQAYAREGV 433
 QY 421 PSEPEPEKVENIGKYTYITWKEIPKSEKGIICNYITFFQAEKGKFSKTWNSIIQYG 480
 DB 434 PSEPEPEKVENIGKYTYITWKEIPKSEKGIICNYITFFQAEKGKFSKTWNSIIQYG 493
 QY 481 LESLKRTSYIVQMASTAGCTNGTSINFKTLFSFVEEITLTLISLGGGLITLITLVA 540
 DB 494 LESLKRTSYIVQMASTAGCTNGTSINFKTLFSFVEEITLTLISLGGGLITLITLVA 553
 QY 541 YGLKRPKLTLHLCPYTPNPAESSIATWGGDFKDKLNLKESDVSVTEDRIKPCSTPS 600
 DB 554 YGLKRPKLTLHLCPYTPNPAESSIATWGGDFKDKLNLKESDVSVTEDRIKPCSTPS 613
 QY 601 DKLYIDLVNFGVNLQEIFTDEARTQGENNLGGEKNG---YVTCF 643
 DB 601 DKLYIDLVNFGVNLQEIFTDEARTQGENNLGGEKNG---YVTCF 643

DB 614 DKLYIDLVNFGVNLQEIFTDEARTQGENNLGGEKNGTRILSSCP 659
 RESULT 9
 ID ABP54363
 AC ABP54363; Protein: 681 AA.
 XX
 XX 20-JAN-2003 (first entry)
 DT
 XX
 XX Human NR10.3 splicing variant protein SEQ ID NO:2.
 DE
 XX
 XX NR10: splicing variant; haematopoietin receptor; immunomodulator;
 KW haematopoietic factor; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation.
 XX
 OS Homo sapiens.
 XX
 XX WO200277230-A1.
 PN
 XX 03-OCT-2002.
 PD
 XX
 XX 22-MAR-2002; 2002WO-JP02769.
 PF
 XX 26-MAR-2001; 2001JP-0087298.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Maeda M, Yaguchi N, Hasegawa M;
 PI
 XX WPI: 2003-018925/01.
 DR N-PSDB: ABO83363.
 XX
 XX NR10 splicing variants of hematopoietin receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases -
 XX
 PS Example 2: Fig 3; 250pp; Japanese.
 CC The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (i) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietin receptor genes participate
 CC in in vivo immunomodulation and haematopoietic cell regulation, and in
 CC the search for haematopoietic factors capable of functionally binding
 CC to the receptors. The present sequence represents the human NR10.3
 CC protein from the present invention.
 CC
 XX Sequence 681 AA:
 SO
 Query Match 87.1%; Score 3405.5; DB 24; Length 681;
 Best Local Similarity 99.1%; Pred. No. 8.7e-280;
 Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
 QY 1 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKSTYQTVKRTYA 60
 DB 33 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKSTYQTVKRTYA 92
 QY 61 FGEHNDCTNNTSSSENKASCSFLLPRTTIPDNTTIEVEANGGVKSHMTYRLNIA 120
 DB 93 FGEHNDCTNNTSSSENKASCSFLLPRTTIPDNTTIEVEANGGVKSHMTYRLNIA 152
 QY 121 KTEPPKIFRVKPVLGIRMIQIEWIKPELAPVSSDLKTYTLRFVNSTSMWEVFAKNRK 180
 DB 153 KTEPPKIFRVKPVLGIRMIQIEWIKPELAPVSSDLKTYTLRFVNSTSMWEVFAKNRK 212
 QY 181 DKNOTYNTLGLQPTFEYVIALRCVAKESKFSWDSOEKMGTEEPACGLELMRVLPAAE 240
 DB 213 DKNOTYNTLGLQPTFEYVIALRCVAKESKFSWDSOEKMGTEEPACGLELMRVLPAAE 272
 QY 241 ADGRRPRLIMKKARGAPVLEKTLGYNIWYPSNTNLTETMTNTNOOLELHLCGESFW 300

```

Db      273  ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMTNTNOOLEHLGGESEFW 332
OY      301  SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVADOLVVKMOSSALDVNTMIMEF 360
Db      333  SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVADOLVVKMOSSALDVNTMIMEF 392
OY      361  PDVDSPTLTSWESVSQATNMTIOODKLRKPCWCYNISVYPMHDKVGEPSYIOAYAKEGV 420
Db      393  PDVDSPTLTSWESVSQATNMTIOODKLRKPCWCYNISVYPMHDKVGEPSYIOAYAKEGV 452
OY      421  PSEGEPTKVENIGKVTYITTKETPKSERKICNTYITFYOEAGGKSKTVNSIIQYG 480
Db      453  PSEGEPTKVENIGKVTYITTKETPKSERKICNTYITFYOEAGGKSKTVNSIIQYG 512
OY      481  LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEIILITSLGGGLIILITLVA 540
Db      513  LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEIILITSLGGGLIILITLVA 572
OY      541  YGLKPKPKLTHLCWPTVPNPAESSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db      573  YGLKPKPKLTHLCWPTVPNPAESSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 632
OY      601  DKLVLDKLVNFGVNLQEIFTDEARTGOENNLGGEKNG--YVACP 643
Db      633  DKLVLDKLVNFGVNLQEIFTDEARTGOENNLGGEKNGTRILSSCP 678

```

RESULT 10

AAB51242
ID AAB51242 standard; Protein: 652 AA.

AC AAB51242;

DT 26-MAR-2001 (first entry)

DE Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.

XX Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;

KM immunoregulation; haematopoietic cell regulation; transmembrane;

KM immune disorder; haematopoietic disorder; autoimmune disease; allergy;

KM metal allergy; pollen allergy.

OS Homo sapiens.

PN WO200075314-A1.

PD 14-DEC-2000.

PF 01-JUN-2000; 2000WO-JP03556.

PR 02-JUN-1999; 99JP-0155797.

PR 30-JUL-1999; 99JP-0217797.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Maeda M, Yaguchi N;

XX WPI: 2001-061720/07.

DR N-PSDB; AAC92337.

XX Hematopoietin receptor protein NR10 for screening potential ligands for

PT treatment of immune and hematopoietic disorders such as autoimmune

PT diseases and allergies -

PS Claim 1; Fig 3-5; 127pp; Japanese.

XX The present sequence represents a human haemopoietin receptor protein

CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane

CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule

CC which participates in immunoregulation and haematopoietic cell

CC regulation in vivo, and is useful in searching for haematopoietic

CC factors capable of binding to the receptor. NR10 can be used for the

CC identification of substances for the treatment and prevention of immune

CC and haematopoietic disorders including autoimmune diseases and allergies

CC such as metal and pollen allergy.

XX Sequence 652 AA:

Query Match 85.7%; Score 3350; DB 22; Length 652;

Best Local Similarity 99.8%; Pred. No. 4.2e-275;

Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MMTWALMLMPLSLCKFSLALPAPENISCYYYRKNLTCTWSGKESTYQTVKRYA 60

14 MMTWALMLMPLSLCKFSLALPAPENISCYYYRKNLTCTWSGKESTYQTVKRYA 73

61 FGEKNDCTNTSSSENASCSPFLPRTIPDNTIEVEANGGVKSHMYRLEIA 120

74 FGEKNDCTNTSSSENASCSPFLPRTIPDNTIEVEANGGVKSHMYRLEIA 133

121 KTEPPKIFRVRPVGLIKRMIOIEMIKPELAVSSDLKYTLFRTVNSTSMVEVPAKNR 180

134 KTEPPKIFRVRPVGLIKRMIOIEMIKPELAVSSDLKYTLFRTVNSTSMVEVPAKNR 193

181 DKNOTYNTLGIQPTVEYIALRCVAKESKFSMDMSQEMKMTBEPAPCGELMRYLPAE 240

194 DKNOTYNTLGIQPTVEYIALRCVAKESKFSMDMSQEMKMTBEPAPCGELMRYLPAE 253

241 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMTNTNOOLEHLGGESEFW 300

254 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMTNTNOOLEHLGGESEFW 313

301 SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVADOLVVKMOSSALDVNTMIMEF 360

314 SMISYNSLGKSPVATLRIIPAIOEKSFQCI EYMOACVADOLVVKMOSSALDVNTMIMEF 373

361 PDVDSPTLTSWESVSQATNMTIOODKLRKPCWCYNISVYPMHDKVGEPSYIOAYAKEGV 420

374 PDVDSPTLTSWESVSQATNMTIOODKLRKPCWCYNISVYPMHDKVGEPSYIOAYAKEGV 433

421 PSEGEPTKVENIGKVTYITTKETPKSERKICNTYITFYOEAGGKSKTVNSIIQYG 480

434 PSEGEPTKVENIGKVTYITTKETPKSERKICNTYITFYOEAGGKSKTVNSIIQYG 493

481 LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEIILITSLGGGLIILITLVA 540

494 LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEIILITSLGGGLIILITLVA 553

541 YGLKPKPKLTHLCWPTVPNPAESSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 600

554 YGLKPKPKLTHLCWPTVPNPAESSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 613

601 DKLVLDKLVNFGVNLQEIFTDEARTGOE 629

614 DKLVLDKLVNFGVNLQEIFTDEARTGOE 642

RESULT 11

AAB51242
ID AAB51242 standard; Protein: 652 AA.

AC AAB51242;

DT 23-SEP-2002 (first entry)

DE Human HPRI variant protein #2.

XX Human; haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;

KM pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;

KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;

KM cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;

KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;

KM osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;

KM anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;

KM demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;

|||||
Db 513 LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEEIIITLSLIGGLIILITVA 572
QY 541 YGLKRP 546
Db 573 YGLKRP 578
RESULT 14
AB05743
ID AB05743 standard; Protein: 764 AA.
XX
AC AB05743;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17-Fc4 fusion protein SEQ ID NO:69.
XX
KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antirheumatic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214935P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;
PI Maurer MF;
XX
DR WPI: 2002-090519/12.
DR N-PSDB: ABA93821.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Example 11: Page 221-223; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antirheumatic, antirheumatic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and AB05730 to AB05745 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 764 AA;

Query Match 71.2%; Score 2783; DB 23; Length 764;
Best Local Similarity 93.8%; Pred. No. 7e-227;

Matches 525; Conservative 2; Mismatches 9; Indels 24; Gaps 2;
QY 1 MMWYALMMLPSLCKFSLAALPAKPNISCVYYRKNLTCTWSPKESYQYTKRYA 60
Db 14 MMWYALMMLPSLCKFSLAALPAKPNISCVYYRKNLTCTWSPKESYQYTKRYA 73
QY 61 FGEKHNDCTNSTSENASCSPFLPRITIPDNTIEVEANGDGVISHMYRLEMA 120
Db 74 FGEKHNDCTNSTSENASCSPFLPRITIPDNTIEVEANGDGVISHMYRLEMA 133
QY 121 KTEPKIFRVPVIGIKRMIOEWIKPELAVSSDLKYLFRFVNSTSMMEVFAKNR 180
Db 134 KTEPKIFRVPVIGIKRMIOEWIKPELAVSSDLKYLFRFVNSTSMMEVFAKNR 193
QY 181 DKNQYNTLGLQPFVEYIALRCVAKESKESQMSQEMKMTTEEPACGLMLRYPAE 240
Db 194 DKNQYNTLGLQPFVEYIALRCVAKESKESQMSQEMKMTTEEPACGLMLRYPAE 253
QY 241 ADGRPPVLLMKKARGAVLEKTLGYNTWYYPESNTNLTETMNTTNOOLEHLGSEFV 300
Db 254 ADGRPPVLLMKKARGAVLEKTLGYNTWYYPESNTNLTETMNTTNOOLEHLGSEFV 313
QY 301 SMISYNSLGKSPVATLRIPAIQENSFOCIEYMQACVADQLVKQSSALDVNTWMEWF 360
Db 314 SMISYNSLGKSPVATLRIPAIQENSFOCIEYMQACVADQLVKQSSALDVNTWMEWF 373
QY 361 PDVSEPTLSMESVSOATNMNTIOODKLPKPCYNISYVPLHDKVGSPYIQVAKRGV 420
Db 374 PDVSEPTLSMESVSOATNMNTIOODKLPKPCYNISYVPLHDKVGSPYIQVAKRGV 433
QY 421 PSEGPETKVENIGVKTIVITWKEIPKSERKGIICNTITFYQAEKGKSKTVNSSILOYG 480
Db 434 PSEGPETKVENIGVKTIVITWKEIPKSERKGIICNTITFYQAEKGKSKTVNSSILOYG 493
QY 481 LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEEIIITLSLIGGLIILITVA 540
Db 494 LESLKRTSYIVQWASTSAGTNGTSINFKTLSPFSVEEIIITLSLIGGLIILITVA 532
QY 541 YGLKRPKNTLHLCMPPTVNP 560
Db 533 --EPRSSDKTHTG--PCCPAP 549
RESULT 15
ABP54368
ID ABP54368 standard; Protein: 549 AA.
XX
AC ABP54368;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.7 splicing variant protein SEQ ID NO:12.
XX
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.
XX
OS Homo sapiens.
XX
PN WO200277230-A1.
XX
PD 03-OCT-2002.
XX
PE 22-MAR-2002; 2002WO-JP02769.
XX
PR 26-MAR-2001; 2001JP-0087298.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
DR WPI: 2003-018925/01.
DR N-PSDB: AB083368.

xx NR10 splicing variants of hematopoietin receptor proteins and encoded
pr genes, applicable in searching hematopoietic factors and developing
pr remedies for immunological and hematopoietic diseases -

Claim 1; Fig 16-18; 250pp; Japanese.

xx
xx
CC The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate
CC in in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.7
CC protein from the present invention.

xx
SQ Sequence 549 AA;

Query Match 70.7%; Score 2764; DB 24; Length 549;

Best Local Similarity 99.8%; Pred. No. 1.7e-225;

Matches 515; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMTWALMLPSLCKFSLAALPAKPENISCVYYRRNLCTWSPCKETSQTYVKRTYA 60
|||
DB 33 MMTWALMLPSLCKFSLAALPAKPENISCVYYRRNLCTWSPCKETSQTYVKRTYA 92
|||
OY 61 FGEKHDNCTNSSTENRASCSEFLPRITIPDNTIEVAENGDCVYKSHMTYRLNIA 120
|||
DB 93 FGEKHDNCTNSSTENRASCSEFLPRITIPDNTIEVAENGDCVYKSHMTYRLNIA 152
|||
OY 121 KTEPKIFRVPVLGIRKMIQEWIKPELAPVSDLKTYLRRTVNSTSMMEVNFAPKNR 180
|||
DB 153 KTEPKITFRVPVLGIRKMIQEWIKPELAPVSDLKTYLRRTVNSTSMMEVNFAPKNR 212
|||
OY 181 DKNQYNTLGLQPTFEYVIALRCVAVESKESKFSWDSQEKMGTEEPGCLMLRVLPAP 240
|||
DB 213 DKNQYNTLGLQPTFEYVIALRCVAVESKESKFSWDSQEKMGTEEPGCLMLRVLPAP 272
|||
OY 241 ADGRPRVLLMKKAGAPVLEKTLGYNWYPESTNLTETMNTNNOOLEHLGSEFPV 300
|||
DB 273 ADGRPRVLLMKKAGAPVLEKTLGYNWYPESTNLTETMNTNNOOLEHLGSEFPV 332
|||
OY 301 SMISYNSLGKSPATLRIPAIQEKSFQCEVWQACVAEDQVVKQSSALDVNTWMEF 360
|||
DB 333 SMISYNSLGKSPATLRIPAIQEKSFQCEVWQACVAEDQVVKQSSALDVNTWMEF 392
|||
OY 361 PDVDSEPTLLSWESVSQATNMTIQODKLKPFWCYNISVYPMLDHVRGEPYSIQAYAKEGV 420
|||
DB 393 PDVDSEPTLLSWESVSQATNMTIQODKLKPFWCYNISVYPMLDHVRGEPYSIQAYAKEGV 452
|||
OY 421 PSEGPEYVENIGVTVITTKETPKSERKGLICNTTIFYQAGGKGSFTVNSSILOYG 480
|||
DB 453 PSEGPEYVENIGVTVITTKETPKSERKGLICNTTIFYQAGGKGSFTVNSSILOYG 512
|||
OY 481 LESLKRKTSYIVQVMASTAGTNGTSINFKTLSPS 516
|||
DB 513 LESLKRKTSYIVQVMASTAGTNGTSINFKTLSPS 548
|||

Search completed: August 4, 2003, 11:22:40
Job time : 88 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:20:42 ; Search time 45 Seconds
(without alignments)
1564.344 Million cell updates/sec

Title: US-09-892-949-2
Perfect score: 3508
Sequence: 1 MMWTWALMLPSLCKFSLAA.....VFARFLVSEKLPHETKGEV 732

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	17.6	917	2	I49699 glycoprotein 130 -
2	682.5	17.5	918	2	A44257 interleukin-6 sign
3	679.5	17.4	918	2	A36337 membrane glycoprot
4	513.5	13.1	783	2	JH0329 granulocyte colony
5	506	12.9	863	2	C38252 granulocyte colony
6	471.5	12.1	837	2	A34898 granulocyte colony
7	443.5	11.3	771	2	B38252 granulocyte colony
8	408.5	10.5	1097	2	SI7308 leukemia inhibitor
9	405.5	10.4	1092	2	JX0312 differentiatin-st
10	242.5	6.2	1162	2	PC4184 leptin receptor, O
11	231.5	5.9	662	2	I13782 IL12 receptor comp
12	231.5	5.9	895	2	S74225 leptin receptor, i
13	227	5.8	1162	2	S68438 leptin receptor, s
14	226	5.7	738	2	I49295 IL-12 receptor bet
15	221	5.7	900	2	S68440 leptin receptor, s
16	219.5	5.6	830	2	I50455 prolactin receptor
17	219.5	5.6	892	2	S68439 leptin receptor, s
18	219.5	5.6	894	2	S68437 leptin receptor, s
19	216	5.5	2222	2	T13924 sck protein - frui
20	207	5.3	636	2	JM0047 class I cytolinase
21	205	5.2	831	2	U10655 prolactin receptor
22	200.5	5.1	610	2	A36116 prolactin receptor
23	199.5	5.1	610	2	A43631 prolactin receptor
24	192.5	4.9	1232	2	T43027 neural cell adhesi
25	191	4.9	292	2	I77525 prolactin receptor
26	191	4.9	303	2	I77524 prolactin receptor
27	191	4.9	310	2	A29884 prolactin receptor
28	191	4.9	608	2	I53269 prolactin receptor
29	188.5	4.8	1898	2	S46216 leukocyte antigen-

30	188	4.8	26926	1	I38344 titin, cardiac mus
31	187.5	4.8	581	2	I45971 prolactin receptor
32	187	4.8	412	2	A41070 prolactin receptor
33	185.5	4.7	1894	2	C54689 protein-tyrosine-p
34	182.5	4.7	1897	1	TDHUK protein-tyrosine-p
35	180.5	4.6	1691	1	D54689 protein-tyrosine-p
36	176.5	4.5	1912	2	A56178 protein-tyrosine-p
37	175.5	4.5	1290	2	A56493 leucocyte common a
38	175	4.5	843	2	A40970 undulin 1 - human
39	175	4.5	6805	2	S20901 titin - rabbit (fr
40	174.5	4.5	1028	2	I58164 Big-1 protein - ra
41	174.5	4.5	1028	2	A53449 plasmacytoma-assoc
42	174.5	4.5	2481	2	A43908 fibronectin - Afri
43	174	4.5	1197	2	T30581 neural cell adhesi
44	171.5	4.4	805	2	S68441 leptin receptor, s
45	171	4.4	1447	2	A54100 tumor suppressor p

ALIGNMENTS

RESULT 1

I49699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
C:Accession: I49699; I48370
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992

A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp
A:Reference number: I48370; MUID:92291532; PMID:1602143
A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: GB:M63336; NID:9193591; PIDN:AAA37723.1; PID:9193592.

A:Accession: I48370

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

RESULT 1

I49699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
C:Accession: I49699; I48370
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992

A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp
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A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I48370

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA4515.1; PID:9840817

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

413 TTPSHVTAAYSVNLKAPKDNLLMVEWTPPPKSVSKYLEMVCVLSNAPCEDVEDMOED 472
414 QATNNTIOODKLKPMWCYNISVYVPLHDKVGEPYSIOAYAKGVPSEGPETKVENIGKT 436
415 ATVNTHLRGLLESEKCYQITVTPFATGPGSESLKAYLKQAPARGPYVTKKVGKNE 532
416 VTIWKEIPKSEKRGIIICNYITFYQAEKGKFSKTVNSSILOYGLESIKRTSYIVQYMA 496
417 AVLAWDOI.PVDDQNGFINRYSISYRTSVGKEMVAVDSSHTEYTLSSLSPTLYMVHMAA 592
418 STSAGCTGTSTNFTLSFSVFEIILITSLIGGGLIILITLVAYGLKPKKHLHLCPT 556
419 YTEDEGKGPETFTTLPKFAOGELEIIVPCLAFLLITLLGLVLCFCKRDLIKKHIPN 652
420 VNPAPSSSIATW-----HGDDPKDKLNLKESDSDS-----VNTEDRLKPCSPSPK 603
421 VPDPSKSHIAQMSPTTPRPHNFNSKDM-----YSDGNFTDVSVLEIANNKKPC--PDDLK 707
422 VIDKLNVNFGVLOEIFTDE--ARTGOENNLG----- 634
423 SVD-----LFKKEKYSTEGHSSGIGSSCMSSSRPSSISSENESSAQSTASTV 755
424 EKNGVYTPFPDPDPLGKSF-----EELPV-----SPEIPPKSKOYL 672
425 EYSTVHSGYRHQVPSVOVFSRSESTOPLDSEERPEDLOLVDSVDSGDELLPRQPYKQ 815
426 S-----RMPEGRPRPEAKCOLLEFSG-----OSLVDPDLCEEGAPN 708
427 NCSQPEACEPISHERSNQVL--SGNEEDFVRLKQOQVSDHISQ-----PY 859

RESULT 2

Interleukin-6 signal transducing molecule gp130 - rat
A:Accession: A44257
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
A:Reference number: A44257; MUID:9305297; PMID:1427893
A:Accession: A44257
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <MAN>
A:Experimental source: liver
A:Note: Sequence extracted from NCBI backbone (NCBI:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 17.5%; Score 682.5; DB 2; Length 918;
Best Local Similarity 27.0%; Pred. No. 3.3e-41;
Matches 214; Conservative 125; Mismatches 339; Indels 115; Gaps 25;

22 PAKPENISCVYYRKNLCTWSPKETSYSY-TQYTVKRYAFGEKHDNCTNSSENRSAS 80
126 PDIFPNTLNCIYNEKKNMLCQDPGRFETLETNTLKSEMA-TEKFPDORTKHGTS----S 180
81 CSF-FLPRTITPDNTTIVEAENGDCVKSMTWRLNIAKTEPKTFKVPVGLIKRM 139
181 CMGCTPTIYFV--NIEVWEAENALGNVSEPIINFDPDKKPKSPPHMLSYTNEEELSSI 238
140 IOIEMIKELPAPVSSDLYTLRFTVNTSGMVEVFAKNRDKQNTYNTLGTQEPTEVI 199
239 LKLAWNSGLDSILR-LKSDIQYRKDASTWIVPL-EDIVSPRTSFTVODLKPFTEVF 296
200 ALRCVAVES--KFWSDSQEKMGTEEPAC-GELMFLVLPAPADGRRPRLMLKARG 256
297 RIR-SIKENCGYMSDSEASGTTIEDRPSKAPSFYKVVANHPQERSRARLWKTLPL 355
257 APVLEKTLGVIWYPPESNTLTETMTNTNOODELHGGESFVWSMISYNSLGKSPVATL 316

356 SEANGKILDEYVLTQSKSVQSYTVNCT--ELIYVLTNNRYVASIARNVYKSPATVL 413
317 RLPALQKSPQCIEMQACVADOLVYKQSSALDVNTWMHMEFPDVDSPTTSLMESVS 376
414 TTPSHFRAASHPVVDLKAFFKDNLLMVEWTPPPKSVKNVNYILEMVCVLSNSPQIPWQED 473
317 QATNNTIOODKLKPMWCYNISVYVPLHDKVGEPYSIOAYAKGVPSEGPETKVENIGKT 436
414 GTVNTHLRGLSLESEKCYLITVTPFATGPGSPSPESKAYLKQAPARGPYVTKKVGKNE 533
415 VTIWKEIPKSEKRGIIICNYITFYQAEKGKFSKTVNSSILOYGLESIKRTSYIVQYMA 496
416 AVLEMDHL.PVDDQNGFINRYSISYRTSVGKEMVAVDSSHTEYTLSSLSPTLYMVHMAA 593
417 STSAGCTGTSTNFTLSFSVFEIILITSLIGGGLIILITLVAYGLKPKKHLHLCPT 556
418 YTEDEGKGPETFTTLPKFAOGELEIIVPCLAFLLITLLGLVLCFCKRDLIKKHIPN 653
419 VNPAPSSSIATW-----HGDDPKDKL--NLKESDSDS--VNTEDRLKPCSPSPK 606
420 VPDPSKSHIAQMSPTTPRPHNFNSKDMYSDANFTDVSVLEIANNKKPC--PDDLKSLD 711
421 KLVNFGVNLQEIFTDE--ARTGOENNLG-----EKN----- 637
422 GYVNCFPFPDPDPLGKSF-----EELPV-----VSPETPKSKOYLBRM 675
423 TVVHSGYRHQVPSVOVFSRSESTOPLDSEERPEDLOLVDSVDSGDELLPRQOYFKQSCS 819
424 PEGTRPE-----AKEOLLEFSGQSLVDPDLCEEGAPNPLYKNSYAREF--L 719
425 QPGASPDVSHRGSSQVPSGSEDEPFLKQOQVSDHISE-----PY--GSDORLRFQSGS 872
426 VSEKLPHTKGEV 732
427 VADALGTGTDCQI 885

RESULT 3

membrane glycoprotein gp130 precursor - human
A:Accession: A36337
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844; PMID:2261637
A:Accession: A36337
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HLB>
A:Cross-references: GH:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C:Genetics:
A:Gene: IL6ST; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 17.4%; Score 679.5; DB 2; Length 918;
Best Local Similarity 28.4%; Pred. No. 5.5e-41;
Matches 175; Conservative 113; Mismatches 261; Indels 67; Gaps 16;

22 PAKPENISCVYYRKNLCTWSPKETSYSY-TQYTVK--RTYAFGE--KHD--NCTTN 71
126 PEKKNLNCIYNEKKNRCEWDGGRFHLNFTLKSEMAHKKRADCKAKRDTPTSCVD 185
72 STSEENRASCSEFLPRTITPDNTTIVEAENGDCVKS-HMTWRLNIAKTEPKTFRV 130
186 YST-----YFV-----NIEVWEAENALKVSDHINFDPYKVV-KPNPPHLSV 230

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QY 131 KPVLGIRKMIQIEMIKPELAPVSSDLKYTLRFTVNSTSMWEVFAKRRDKNOTYNLG 190
D 231 INSEELSSILKLTWNPNSIKSVII-LKYNQYRTKQASTSQIP-PEDTATSSSFTVOD 288
QY 191 LOPPEYVALRCVAVESK-FMSDWSOEKMGTEEEAPC-GLEMLRVLKPAEADGRPRV 248
D 289 LKPFTEVFRICMKEDGKGYMSDSEASGITYEDRPSKAPSEFWYKIDPSHQGYRTVQ 348
QY 249 LMKKARGAPVLEKTLGYNIWYRPESNTNLEFMNTNNOLEHLGEGSEWVSISNSL 308
D 349 LVMKTLRPFPEANGKILDIYEVTLRKMSHLONVYNAT--KLTVNLMDRYLATITVRNLV 406
QY 309 GKSPVALTRIPALQESFOCIEVWQACVADOLVKKQSSALDVNTMMIMFDPVDSEPT 368
D 407 GKSDAVALTIPACDFQFHFVMDLKAPKDNMLMVEITTPRESKKATILEMVCVLSDKAPC 466
QY 369 TLMSEVSQATNNITQODKLKPFMCYISVYPMHLKVGEPYSTQAVAKGVSEGEPTK 428
D 467 ITDMQOEDCTVHFHYTLGKGLAESKCYLITVTPVADDPGSPESIKAKVAPPSKGPVTR 526
QY 429 VENIGVTVTITMKEIPKSEKGIICVYTLFQAEKGKFSKTVNSLLOGLSLKRT 488
D 527 TKVGNKEAVLENDQLEVDVQNGFIRNYTTLFRTIGNETAVNVDSHTEYTSLSIDPT 586
QY 489 SYIVQVASTSAGTNGTSINFKLSFVFEIILITSLIGGLLILITLVAYGLKRPNK 548
D 587 LYVWMAAYTDEGKDEPFTTPPKAAGEIEIAIVPVCLAFLLTLGLVLPFCNKRDL 646
QY 549 LTHLCWPTVPNPAESSIATW-----HGDFKDKL----- 577
D 647 IKHIMVNPDPSPSHIAQMSPTPRHFNFSKDMQYSDGNFTDVSVEIEANDKKPPE 706
QY 578 NIKESD-----DSVTE 589
D 707 LKSLDLFKKKEKINTE 722

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RESULT 4

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JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757; PMID:2147944
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <LAR>
A:Cross-references: GB:X55720; NID:g31698; PIDN:CA39252.1; PID:g31699
A:Experimental source: Placenta
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-783/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 13.1%; Score 513.5; DB 2; Length 783;
Best Local Similarity 26.8%; Pred. No. 4.9e-29;
Matches 195; Conservative 95; Mismatches 278; Indels 159; Gaps 34;

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RESULT 5

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JH0329
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; A38252; JH0330; A46486; S66332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348; PMID:1701053
A:Accession: C38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FKR>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A:Note: clones pHC11 and pHC5
A:Accession: A38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone pHC3
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757; PMID:2147944
A:Accession: JH0330

```

RESULT 5

```

QY 130 VKPVLGIRKMIQIEMIKPELAPVSS-----DKYTLRFTVN--NSTSMWE 172
D 235 MDP-----SPEAPRQAGCLOQCEWEPQGLHINQKCELRHHPQGEASMAL 281
QY 173 VNFANKRDKNNQYNLGTLOPTEYVALRC-AVKESEFMSDWSOEKMGTEEEAPC-CGL 230
D 282 VG---PLPLALQELCGLLPATVATLIQICIRIPLEIGHMSDMSPSLELTTERAPVRL 338
QY 231 ELW---RLKPAEADGRPRVLLMKKARGAPVLE---KITGYNWYRPESNTN-LTETPN 283
D 339 DTMWRQOLDP-----RTVQLEKRP--VLEEDSGRIQGYVSWPSCQAGAILPLCN 389
QY 284 TTNOLEHLGEGSEFWVSMSYNSLGKS---PV--ATLRIPALQESFOCIEVWQACVAE 338
D 390 TTLSCTCFHLPSAEQVALVAAYNAGTSRPTPVVFSRSRQALURLH-----AMAR 440
QY 339 D--QLVKKQSSALDVNTW-----MIEFP---PDVDEPTLLSMESVSQATNNITQODKL 389
D 441 DPHSLWGWMEPP-----NPMFQGYVIEWGLGPPSASNSNKTWRMQRNGRATGFLKEN-IR 495
QY 390 PEMCYNISVYPMHLKDKVGEPYSTQAVAKEGVSEGEPTKENTIGKVTITMKEIPKSER 449
D 496 PQLTEITVTPLODTMGPSOHVAYISQEMAPSHAPLHLKHGKTWAQLEWPEPELG 555
QY 450 KGIICNTYIPQAEKGKFSKTVNSLLOGLSLKRTSYIVQVASTSAGTNGTSIN 509
D 556 KSPILHTYITWNTNQNQSFALINASSRGVHLHLEPASLYHLHMAASQAGATNSVLT 615
QY 510 FKLSFVFEIILITSLIGGLLILITLVAYGLKRPNKLTLCWPTVPNPAESSIATW- 568
D 616 LMTLTPGSELIHLGLFGLLLTLCGTAMLCCSPNRKRP-LWPSVPPAHSSLSGSW 674
QY 569 -----HGDFK-----DKLNKESD-----DSVNTEDRLKCPSPDGLVDKL 608
D 675 PTMEEDAFOLPGIGTPPTTLVLEDEKKVPWESHNSE---TCGLPT-----L 723
QY 609 VVNFQVLOEIFTDARTGOENNLGCKNGVYTCPPDPCLGKSFEEELPSPPIPPRS 668
D 724 VQRY--VLQ-----GDPRAVST---QPGQSGS-----DQAGPPRRS 756
QY 669 QYLRSM 675
D 757 AYFKDQI 763

```


Db 716 SG--NGSLPALVQAVYLGDPREISNOSQPPSRFGDVLVGVLESPFSGV---MQYI 769
OY 672 RSRMEGRNP 681
Db 770 RS---DSTDP 776

RESULT 7

B38252
granulocyte colony-stimulating factor receptor precursor (clone pHQ2) - human
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 05-Nov-1999
C:Accession: B38252
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor receptor
A:Reference number: A38252; MUID:91062348; PMID:1701053
A:Accession: B38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-771 <PUNK>
A:Cross-references: GB:M59819; GB:M38026; NID:9485363; PIDN:AAA63177.1; PID:9485364

Query Match 11.3%; Score 443.5; DB 2; Length 771;
Best Local Similarity 25.4%; Pred. No. 5.7e-24;
Matches 189; Conservative 90; Mismatches 297; Indels 169; Gaps 34;

OY 22 PAKENISCVYYRKNLT-----CTWSBGETSY--TOYTKRYTAFGEKHNDCTNNSST- 74
Db 123 PAIHNLSCLE---MNLTSLLICOMEGEPETHLPTSTFLKSPKRS---NCOTGDSI 174
OY 75 -----SENBRASCFFLPRTIPDNVTTEVEAENGQGVKSHMTYRLNIAKTEPKIFR 129
Db 175 LDCVPKQGSQSCIPRKHLLIYQMMGLWQAHNGLTSMSPQLCDPMDVVKLEPPMILT 234
OY 130 VKPVLGIRMIQIEIKPELAPVSS-----DLKTYLRFRTV--NSTSWE 172
Db 235 MDP-----SPEARPOAGCLOLCWEPWQPLHINOKELHNRKQGRGASVAL 281
OY 173 VNFKNRKDKQNTNLGLQPTFEYVIALRC-AVKESFWSMDSOEKKMGTEEARP-CGL 230
Db 282 VG---PLPEALQYELGGLPATYTLQIRIRPDLPGHWSMDSSLELRTTERAPTVRL 338
OY 231 ELW---RYLKPAEDGRPRVLLMKKAGAPVLE---KTLGYNIMYIPESNTN-LTETMN 283
Db 339 DTWKRQOLDP-----RTVQLFMPK---VPLEEDSGRIQGYVSWRSGQAGAILPLCN 389
OY 284 TTNOQLHLHGSEFWWSMISNLGKS--PV--ATLRIPAIOEKSFQCIENVQACVAE 338
Db 390 TTELSCTFHEPSEAOEVALVANSAGTSRPTPVFSESGPALTRLH-----AMAR 440
OY 339 D--QLVYKMOSSALDVNTM---MIEWF---PDVDSEPTTILSWESVSQATMTTQOQK 389
Db 441 DPHSLWGWEP---NPMPOGYVIEWGLGPPSASNSKRTWRMEONGRATFLLEKEN-IR 495
OY 390 PFMQYINISVYPMLDKDGEPYSIOAYAKEGVSEGPENKVENIGKVTITIMKEIPKSR 449
Db 496 PFOLEIITVPLVYDTPGSOHVAIYSEMAPSHAPLHLKHIGKTAQOLWVPEPPLG 555
OY 450 KGIICNTIIFYQAGGKGFSTVNSILQYGLSIRKRTSYIVOMASTAGTNGTSIN 509
Db 556 KSPILHTIIFWTNQNQNSFALINASSRGFVLHGLEPASTLHILHMAASQAGATNSTYL 615
OY 510 KFTLSFVSFEIILITSLIGGLIILITVAVGLKPP---NKLHLKCPYTPNPAESSIA 566
Db 616 LMTLTPAP-----TGRIPGOVSOTQTLTAAWAPCCPQSWMRMPSSCPALRHSPSS-Q 668
OY 567 TWHGDDFKDLNKESDSDSVNTEDRILKPCSTPSDKLITDLVNVFNGVLEIFDEART 626
Db 669 CW-----RRMKRSRCPGSPITIAQRPVAS----- 691
OY 627 GOENNLGEGKNGYVTCPE--RPDCPLKGSFEEPLVSPETIPPKSQILRSRME-GRPEA 683

Db 692 -----PLMSRPMCSRQVQ--EQPPSPN--PSLAPAIRSFGSCWAPQA 732
OY 684 KEQLLFSGQS-LVPHDLCEBAGAPNP 707
Db 733 QGGGTISAVTPLSPSWRASPPAPSP 757

RESULT 8

S17308
leukemia inhibitory factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S17308
R:Gearing, D.P.; Thut, C.J.; Vandembos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Pr
EMBO J. 10, 2839-2848, 1991
A:Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 sign
A:Reference number: S17308; MUID:92007727; PMID:1915266
A:Accession: S17308
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1097 <GPA>
A:Cross-references: GB:X61615; NID:934365; PIDN:CAA43805.1; PID:934366

Query Match 10.5%; Score 408.5; DB 2; Length 1097;
Best Local Similarity 21.3%; Pred. No. 3.4e-21;
Matches 178; Conservative 139; Mismatches 292; Indels 225; Gaps 40;

OY 22 PAKENISCVYYRKNLTCTWSBGETSY-----TOYTKRYTAFGEKHNDCTNNSSTSE 76
Db 333 PDTPQQLNCETHDKLEIKISWNPGRVTLVGPRTSYTLVESFS-GKYVRLKRAEAPNE 391
OY 77 NRASCFPLRPIITIPDNVTIEVEAENGQGVKSHMTYRLNIA-KTEP--PKIFRYKPV 133
Db 392 SYQLFQMLPQOEL---YNFTLNAHNPGL--RSQSTI--LVNITEKYVPHPTSEKVDI 444
OY 134 LGIRKMIQIEIKPELAPVSSDLKTYLRFRTVNSTSWEV---NEAKNRK-----KNQ 184
Db 445 --NSTAVVLSMHLG-----NFAINFLCELEIKNSVQGRVNTIKGVENS 490
OY 185 TY--NLGLQPTFEYVIALRCVAKESKFSWSQSOEKKMGTEEARP-CGLEIMRYLKPAEA 241
Db 491 SYLVALDKLNTYTLTYTERIRCTEFTFWKMSKMKQHLTTEASPSKPDTPWR---EWS 547
OY 242 DGRPRVRLMKKAGAPVLE---KTLGYNIMYIPESNTNLTETMTTNOQLHLHGSEF 298
Db 548 DGNKLI-LYMKP---LPINEANGKILSYNVCSSDEETQSLSEIPDQHKAEIRLDKNDY 603
OY 299 WWSMISYNSLGKSP---VATLRIPAIOEKSFQCIENVQACVADQLVYKMOSSALDVNTM 355
Db 604 IISVYAKNSVSSPSKRIASMEIPNDLKIQVVMGKG-----ILLTMHYDPRMTCDY 657
OY 356 MIEWPPVDSEPTTILSWESV--SQATNMTTQOQKLPFCYNISV-----YPMLDKVG 407
Db 658 VIKMNCSSRSRSPCLMDMKRVPNSSTETVIESDEFPRGRVNFPLGYCRNQGQYLLRSMIG 717
OY 408 EPTSGAARAKGVPSEGETVVENIGVTVITTKELIKSRKGLICNYITIFYQAGGKG 467
Db 718 -----YIEELAPVAPNFTVEDTSADSLVKKWEDIVEELRGFLRGLYLF---GKG 766
OY 468 FSKTVNSILOYG-----LESIRKRTSYIVOMASTAGTNGTSIN 509
Db 767 ERDTSKMNVLBSGRDIDKVNITDSOKTLADOGKTSIHLVIRATITDDGVGPEKMY 826
OY 510 KFTLSFVSFEIILITSLIGGLIILITVAVGL-----KPNKLTHLCPVTP 558
Db 827 VVTKENSV-----GLITAILIPVAVVIVGVTSILCYRKREMIKETFEYDIP 874
OY 559 NPAESSITWHDGDKDLNKESDSDSVNTEDRILKPCSTPSDKLVID----- 606
Db 875 NPENCKALOQ-----QKSYCEGSSALKTLE--MNPQ-TNNNEVLELTRSAFPKIEDTE 924
OY 607 -----KLIVNP-----GNVLOEIFTD----- 622

Db 925 IISPAEREDSDAEPENHVAVSYCPPIIEEIPNPADEAGCTAQTIVIDVQSMYOPQ 984
 QY 623 -EARTGOENN-LGSGKNGVYTCFPRPD--CPLGKSEELPVSPETPRKRSQVLRSMRPG 678
 Db 965 AKPEEODNPVGA--GY-----KQMLPLNSTVEDIAEEDID-----KTAG 1027
 QY 679 TRPEAKQOLFSGQSLVPD-----HLCBGAHPNPLKNSVTAREFLVSEK 723
 Db 1028 YRPQAN---VNTWNLVSPDSPRSDSNSEIVSFGSP-----CSINSRQFLIPPK 1073

RESULT 9

JX0312
 differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor - mou
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1985 #sequence-revision 07-Oct-1994 #text-change 01-Dec-2000
 C:Accession: JX0312; J02181; S38942
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
 J. Biochem. 115, 557-562, 1994
 A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
 A:Reference number: JX0312; MUID:94334302; PMID:8056772
 A:Accession: JX0312
 A:Molecule type: mRNA
 A:Residues: 1-1092 <TOM>
 A:Cross-references: DDBJ:D26177; NID:9473718; PIDN:BA05165.1; PID:d1005707; PID:9825506
 A:Accession: J02181
 A:Molecule type: mRNA
 A:Residues: 1-717, 'EA' <TOM1>
 A:Cross-references: DDBJ:D17444; NID:9441493; PIDN:BA04258.1; PID:d1004778; PID:9441494
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
 FEBS Lett. 334, 193-197, 1993
 A:Title: Pregnancy associated increase in mRNA for soluble D-factor/LIF receptor in mous
 A:Reference number: S38942; MUID:94039833; PMID:7901054
 A:Accession: S38942
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-717, 'EA' <TOM2>
 A:Cross-references: GB:D17444; NID:9441493; PIDN:BA04258.1; PID:d1004778; PID:9441494
 C:Keywords: differentiation; receptor; transmembrane protein
 F:1-43/Domain: signal sequence #status predicted <SIG>
 F:44-1092/Product: differentiation-stimulating factor/leukemia inhibitory factor recepto
 F:828-854/Domain: transmembrane #status predicted <TM>

Query Match 10.4%; Score 405.5; DB 2; Length 1092;
 Best Local Similarity 21.7%; Pred. No. 5.6e-21;
 Matches 180; Conservative 131; Mismatches 304; Indels 213; Gaps 36;

QY 22 PAKPENISCVYYRRKRLTCTWSPKETSYS-----TOYTV-----KRT 58
 Db 328 PDVPOKLCEETHDLKEIICSNWPGRTGLVGRNTEYTLFESIGKSAVFRIEGLTNET 387
 QY 59 YAFG-EKDNCTNSTSENRSASCFILPRITIPNTIIEVAGNDGIVKISHMYWLE 117
 Db 388 YRLGVOMHPGGEIHFFLTJGR-----NPLGQASAVVINTE 424
 QY 118 NIAKTEPKIRFVPLGKIRMIQIEWIKPELAPVSDKLYTLRPTVNSMMEVNPFAK 177
 Db 425 RVAHPDPTSL-KVNDI--NSTVYTFESWYLPG-----NFKINLNLQIETICAN 469
 QY 178 NRKD-----KNQYVNTL--GIQPTVEVIALRCVAKESKESQEMKMTTEEA 226
 Db 470 SKKEVRNATIRGAEDSTYHVAVDKLNPTAYTFVRVRCSSKTFMKWSRMSDEKRHLTTEAT 529
 QY 227 PC-GELMRVLKPAEADRRVRLMKARCAPVE---KLGVIWITYPESNTNLTETM 282
 Db 530 PSKGDVTR---EWSDDKNLI-YWKP---LPINEANGKILSYVSCSLNEETQSVLEI 582
 QY 283 NTKNOLELHKGESFVSMISYSLGSP---VATLRIPALIOKSFQCIEMQACVAD 339
 Db 583 FDPQHRARITQLSKNDYIISVAVARNAGSSPSKIASMEIPN-----DITVEQAVGLGN 636

QY 340 QLVAKMOSSALDVTNMTIEMFPDVDEPTLSMESV-SQATNMTIQODLKPFMCYNISV 398
 Db 637 RIFLTHRDPMNMTCTCYVIAKMCNSSRSEPCLLDMRVRVPSNSTETVIESQFGQVGRNYL 696
 QY 399 YPMLHDKGEPISQIAYAKEVPSSECPETKVENICVYTTWKETIPKSEKGIICNTI 458
 Db 697 YGCTNOGYQLNRSIIIGVEELAPVAPNTEVDTSADSLVYWDIIPVEELGFLRGY-L 755
 QY 459 FYQAGGKGESKT-----VNSLLOYGLESKRTSYIQVMASTAG 501
 Db 756 FYQKGERDPTKTRBLEPHRHSIDIKLKNITDISQKTLR--IADLQKTSIHLVLRATYHGG 813
 QY 502 GTNGTSINKEKTLFSVFELLITLSLGGGLLILITVAYGL-----KRPKNLT 550
 Db 814 LGPEKSMFVTVKENSIV-----GLITAILIPVAVAVYGVVSIILCRRENIK 861
 QY 551 HLCWPTVVRPAESSIATWHGDDFKKLNLKESDSDVNTEDRLKCSIPSKVLVD--KL 608
 Db 862 ETEYEDIPNPENCKALQF-----QKSVCEGSNALKTLE--MNC-TPNNVEVLESRSI 911
 QY 609 VVNFQNVLOEIPPTDEA-RTGOENNLGEGKNGVYTCP-----PRPC----- 648
 Db 912 VPKIDT--EITISPAERPERGENSEVDPENHVAVSYCPPIIEEIPNPADEAGCTAQTIV 969
 QY 649 -----PLKSFEE-----LPVSPETIPPKRSQVLRSMRPECTRPAK 684
 Db 970 IDVQSMYOPQAKAEEDQVDVAVAGYKQMLPLSPAVEDTAADEGK--TAGYRPQAN 1028
 QY 685 EQLFSGQSLVPD-----HLCBGAHPNPLKNSVTAREFLVSEK 723
 Db 1029 --VNTWNLVSPDSPRSDSNSEIVSFGSP-----CSINSRQFLIPPK 1068

RESULT 10

PC4184
 leptin receptor, Ob-Rb - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Aug-1996 #sequence-revision 13-Mar-1997 #text-change 01-Dec-2000
 C:Accession: J04895; J04896; J04897; PC4184; J04797
 R:Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta
 Biochem. Biophys. Res. Commun. 225, 75-83, 1996
 A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi
 A:Reference number: J04895; MUID:96332408; PMID:8769097
 A:Accession: J04895
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1162 <TAK>
 A:Cross-references: DDBJ:D85558; NID:91526441; PIDN:BA12831.1; PID:d1013515; PID:g15
 A:Accession: J04896
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 1-796, 'G', '1157-1158', 'TVLLN' <TA3>
 A:Cross-references: DDBJ:D85559
 R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
 Biochem. Biophys. Res. Commun. 224, 597-604, 1996
 A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
 A:Reference number: PC4184; MUID:96295531; PMID:8702432
 A:Accession: PC4184
 A:Molecule type: mRNA
 A:Residues: 840-1162 <IID>
 A:Cross-references: DDBJ:D84550
 R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
 Biochem. Biophys. Res. Commun. 222, 19-26, 1996
 A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f
 A:Reference number: J04797; MUID:96212906; PMID:8630068
 A:Accession: J04797
 A:Molecule type: mRNA
 A:Residues: 1-889, 'RADTL' <I12>

A:Cross-references: DDBJ:D84125; NID:91374707; PIDN:BAAL2230.1; PID:91374708
 A:Experimental source: adipose cell
 C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa) rat
 C:Genetics:
 A:Gene: fa
 C:Keywords: appetite; transmembrane protein
 F:840-860/Domain: transmembrane #status predicted <TM>
 F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 6.2%; Score 242.5; DB 2; Length 1162;
 Best Local Similarity 22.0%; Pred. No. 4.2e-09;
 Matches 170; Conservative 99; Mismatches 305; Indels 199; Gaps 42;

```

27 NISC-VYYRKNLCTWSPGKETSYQYTKRYAFGEKHDCNTNS---TSENRAAC 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 NISCETGTYLTKMCRSPSTIOSLVSTVOLRY--HRSILYCPDNISIREPTEK-NCV 487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82 -----SFLPRITIPDNTYIEEANGDGVKSHMTYRLNENIAKTEPPKIFRYKPV 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
488 LQDGFEECYRQF-IFLISGYTWMIRINHSLSLSDPTCVLPDSYVKKPLPPS--NYKAE 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
134 LGIR-MIQEWMIPELAPVSSDLKYTLRFPTVNSTSMVEYNFAKNKQNTYNLTGLQ 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
545 ITINTGLKVSWEKPPVP--ENNLOFQIRYGLNGKEIQMKTHEVFDAKSKASLPVSD- 601
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193 PFEYVIALRCVAKES-KFMSDSQEKMGW-EEAPC-GLELWRLKPAADGRPRVRL 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
602 -CANYVQVRRLDGLGIVSNMSSPAYTLMDVKVPRGPEFRIMDGTIKKERNTL 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
250 LMK-----KARGAPVLEKTLGVNIWYPSN-TNL-ETMNTNQLLEHLGG 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
661 LMKRLMKNDLSVRYRYVKHRTAHNGTWSQDVGNQNLFLFMAESATVIV-----LAI 715
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
296 ESFVSMISYNSLGSVPATIRIPAIQEKSPQIEVMQACAEOLVYKQSSALDVNT- 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
716 NSIGASLVNENLTFSPMS--KVNAVQ--SLSAVPLSSCV-----ILSWLSNDYSL 766
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
355 -WMIEW--FPVDSEPTLLSWESVSQATNMTIQQDKLPFCWYNISYVPMHJHVGEPYS 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
767 YLVIEKMLNDDDG---MKYLRIPSNVKNKYIHDNFIPIKQPSLYPVMIEGVGKPI 822
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
412 IQAYAKGVPSGEPE-----TKVENIGVKTYT-----ITWKEIPKSEKGI 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
823 INGTCKDIKQONDAGLYVLPITISSCVLLGTLLISHQRMKFLFMDVDPNPKN---- 878
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
454 CNITIFFOABEGKGFSTVNSIIQYGLSKKRTSYIVQMASTSAGTNGTSINFKTL 513
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
879 CSMA-----QGLNFQKPEP----- 892
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
514 SFSVEEILL--ITSLIGGLI-----LIITLVAGLKK--PNKLTILCWPVYNP 560
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
893 -----FEHLFTKHAASVIFGPLLPEPVPSEISYDTAKKNKDNVAPMAVSL-TPDS 947
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
561 AESSIAIWMHGDGFKDKLNLESDDSVTEDRILKPC-STPSDKLVIDKLVVNGVNOEI 619
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
948 TRGSIC-----ISDQCSANFSGAOSTGCEDECOSQSVKVA--TLVSN-----YKT 995
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
620 FTDAKRGQENNLGKNGVYTCPPRPDCLPKSFELPVSPETLPKRSQTLRSRMPEGT 679
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
996 ETDEEQ-----GAIHSSVOCIAKHSPLRQSFSS--NSMEIEAQAFLLSDHPPVVI 1046
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
680 RPEAKEQILFSGSLVDPDLCE-EGAPNPYLKNSVTAREFLVSEKLEPHETKGE 731
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1047 SP-----QLSFSGL-----DELLELG-----NFPENHGE 1072
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 11
 137892
 I12 receptor component - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: 137892
 R:Chua, A.O.; Chizomile, R.; Desai, B.B.; Tuit, T.P.; Nunes, P.; Minetti, L.J.; Warr

J. Immunol. 153, 128-136, 1994
 A>Title: Expression cloning of a human IL-12 receptor component. A new member of the
 A:Reference number: 137892; MUID:9426217; PMID:7911493
 A:Accession: 137892
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-662 <RES>
 A:Cross-references: EMBL:U03187; NID:9507150; PIDN:AA21340.1; PID:9507151

Query Match 5.9%; Score 231.5; DB 2; Length 662;
 Best Local Similarity 21.7%; Pred. No. 1.1e-08;
 Matches 149; Conservative 96; Mismatches 253; Indels 189; Gaps 34;

```

8 WMLPSLCKFSLALPAK-----PENISCYIYKKNLTCWSP 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 WVPVLLFLFLSLRGACRTSECCFQDPYPADSGASGRDLCYRISSDRYECSMQY 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
45 GKETSQYQYTKRYAFGEKHDCNTNSSTENRASCSEFLPRITIPDNTIE--VPAEN 102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 EGPTAGVSHFLRCLSSG-----RCQYFAAGSATPLQ--PSDQAGVSLTYTLTLMVESA 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
103 GDGVKSHMTYRLNENIAKTEPP-KIFRYKPVIGIKRMIOLEWIKPELAPVSSDLKYTLR 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 RNQTEKSPREVTLQLYNSVKYEPPLGDIKSKLAGQLRM--EMETPD-NQVGAEEVF--R 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 FRTYNSTSM-----MEVFAKNRKDKNOTYTLGLQPTFEVIALRC 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 HRT-PSSPMKLGDCPODDDTESCLCLEMNAQ-----FEQLRRQ 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
204 AVKESKFWDSQ-----EKNG-----MTEEAPCGLELWRLKPA 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
215 LGSQSSMSKSSSPVCPPEPNPQYRFVSQJGQGRRLTLKEQPTQEL-----PE 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 EADGRPVRLMKARGAPVLEKTLGVNIWYPSNLTLETMTNQLLEHLG----- 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270 GCOGL-----APGTEVT--YRLQHLMLSCPCAKAKART-----LHGGKMPYL 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 -GESFVSMISYNSLGSVPATIRIPAIQEKSPQIEVMQACAEOLVYKQSSALDVN 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
310 SGAATNVAIVSNQFQELNOTWHIPADTHTEPALNI--SVQNGTMTWAPRAQSM- 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
354 TWMIETWP-----DVDSEP--TTLWSVESQATNMTIQQDKLPFCWYNI 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
366 TYCIEMQPVGGDGLATCSLAPQDDPDAGMATWSMESGA-----WGQEK-----CYI 416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
397 SVYPLMDKGEPPS--IQAY-----AKGVPSGEPTKVENIGVKTYITWKEIPKSE 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
417 TIFASAPHEKLTLMSTVLSYHFQGNASAGTPH--HVSYKNSHSDSVDMAPSLIST 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
449 RKGIIICNTIYQABEGGKGFSEK-TVNSIILQYGLSKKRTSYIVQMASTS-AGTNGT 506
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
474 CPGLVLEKVVACRQEDSKQVSEHPQPTQVTLISGLAGVAYVQVADTAMLRGWSQ 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
507 SINKTISFSVEEILLITSLIGGLIILITLVAY-GLKRPNKTLHLCWPTVPAPASSI 565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
534 PQRF-SIEVQSWDLIFPASFSGFLSILLYGVLTGLNRRAR--HLC-PLLPFPCASSA 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
566 ATWHD-----DFKDKLNLES 582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
590 IEPFGKETWQINPVDFOEASLOEA 616
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12
 S74225
 Ieptin receptor, isoform Ob-Rf - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
 C:Accession: S74225
 R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
 FEBS Lett. 392, 87-90, 1996
 A>Title: A novel leptin receptor isoform in rat.
 A:Reference number: S74225; MUID:96368027; PMID:8772180
 A:Accession: S74225

A:Molecule type: mRNA
 A:Residues: 1-738 <RES>
 A:Cross-references: EMBL:U02922; NID:g1046233; PIDN:AAA87457.1; PID:g1046234

Query Match 5.8%; Score 226; DB 2; Length 738;

Best Local Similarity 20.1%; Pred. No. 3.3e-08;
 Matches 163; Conservative 113; Mismatches 309; Indels 224; Gaps 37;

```

OY 22 PAKENISCVYYKKNLCTW---SPKETSITQYTVKRTAFGKHNC---TINSST 75
DB 45 PLGRPNLSCYKSVKTDYECSSWQYDGPEDNVSHVLMC-----CEVPPNHTTG 91
OY 76 ENRASCSEFF-----LPRITPDNTTIEEAENGCVIKSHMTYRLNIATKE 123
DB 92 QER---CRYFSSGPDRTQYFQWEDGIPVLSKYNFVWESLGRNTRKMSQKISQYLVMWTTT 149
OY 124 PPKIFRYKPVLGIRKMIQIENIKPELAVSSDLKTYLRFRTVNSTSMMEVFAKRNKDN 183
DB 150 PP-LGHK-KVSQSHQQLRMDV-----NVSEBAGAEOVFRFRMPPTN 188
OY 184 QTYNLTGQPTT-EVYIALRC-AVRESKF-----WSDWS 215
DB 189 WTLGDCGQVNVSGVGLDIDGSSMSCLCPSENMAOEIQRRLSSGAPGCPWSDMS 248
OY 216 QEKMGTEEEAPCGLELWRLVLPADGR-----PVRLMKKARGAP-----V 259
DB 249 M-PCVPEVLP-QAKIKELVEPLNOGRRRLTMGOSPOLAVPEGCGRCQAQYKRLV 306
OY 260 LEKTLGIWYIPESNTNLTMTNTNOOLELHGESFWWSMISYNSLGSVPATLRIP 319
DB 307 LVRLM-----SCRCQOTSKTVPPLGKLNLSGATYDLNLAKTRFGSTIQKMLP 357
OY 320 AIOEKSFQIEVMAQVADOLVYKWSALDVNTMTMEMP-----D 362
DB 358 AOELTETALV---SVGNNMTSMQMAQA-PGTYCLEQWQFQHRNHTTCTLIPREE 413
OY 363 VDSEPTLWESVSQATNWTIQODKLPFCWYNISVY-----PMLHDKVGEPSIOAY 415
DB 414 DPAKAVTHWSMSKP-----TLEQE-----CYRIVFAKSNKPNKMLATVLSYFQGN 463
OY 416 A-KEVSESEGPETKVENIGVTVTITKEIPKSEKGIICNTIITYOAEQGGKFSK-TVN 473
DB 464 ASRAQTPR---HVSVRNOTGDSVSVEWTASQSLCTCPGLTVQVYVCEAEDGAMSEMLVP 520
OY 474 SSIIQGESLKRKTSYVOVMASTASAGTNGTSINFKTLSPV---FELLITSLIGGL 531
DB 521 PTKTOVTLIDGLRSRVMYVOYRADTAR--LRGAMSHPRFSFEVOISRSITIFASLGSFA 578
OY 532 LILILIVAY-GLKKPNKLTFLCPTVPNPASSIATWHDGDFKDLMLKESDSDVNTED 590
DB 579 SVLLVGSIGYIGLNR-AAAMHLC-PPLPTPGSTAVEFPGSG-----KQAMQMCNPD 629
OY 591 RLKACSTPSDKLVLDKLVNFGVNLQELFTDEARTGOENNGEKNQVTCPPRPDCL 650
DB 630 --FPEVLYPRDALVE-----MPGDR----- 648
OY 651 KGSFELVSPETIPRKSOYLRSMBEGTRPAKROLLFSQGSILVPHLCEGAPN----- 706
DB 649 GDGTESPOAAPBCA-----LDTRRPLEFOROVALSEARL---GLAREDCPRGDLA 699
OY 707 ---PYLKNVYAREFLVSEKLPENTKE 731
DB 700 HTVLPILLGCVTQGASVLDLMTHTKTA 728

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RESULT 15

568440

leptin receptor, splice form Ob-Rd - mouse

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000

C:Accession: S68440

R:Lee, G.H.; Piroenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fu Nature 379, 632-635, 1996

A>Title: Abnormal splicing of the leptin receptor in diabetic mice.

A:Reference number: S68437; MUID:96231997; PMID:8628397

A:Accession: S68440

A:Molecule type: mRNA

A:Residues: 1-900 <LEE>

A:Cross-references: EMBL:U49109; NID:g1195490; PIDN:ACS2423.1; PID:g1195491

A:Experimental source: tissue hypothalamus

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

C:Keywords: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR: F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 5.7%; Score 221; DB 2; Length 900;

Best Local Similarity 20.0%; Pred. No. 1e-07;

Matches 119; Conservative 86; Mismatches 219; Indels 172; Gaps 26;

```

OY 27 NISC-VYYRRNLTCTWSPKETSITQYTVKRTAFGKHNCNTNS---TSENKASC 81
DB 431 NISCETDGYLTRKTCRMSPTTQSLVSTVOLRY--HRSLYCPDSPSIHPTSEPK-NCV 487
OY 82 -----SFLPRITPDNTTIEEAENGCVIKSHMTYRLNIATKEPKIFRYKPV 133
DB 488 LQROGFYCVQOP-IFLLSGYTMIRINHSLSGSDSPPTCVLPDVSVPKPLPS--NVKAE 544
OY 134 LGIRK-MIQIENIKPELAVSSDLKTYLRFRTVNSTSMMEVFAKRNKQTYNLGLQ 192
DB 545 ITVNTGLGLVSEKVEFP--ENNLQFOIRYGLSCKEIQMKTHEVADAKKSASLSVSD- 601
OY 193 PTEVYIALRCVAKES-KFWSQWSQEKMGMT-EEAPC-GLELWRLVLPADGRGRRVRL 249
DB 602 -CAVTVQVRCRRDLGLQISWSSSPAYTLVMDVAVPARGPFRMKMGVTKERNVTL 660
OY 250 LMK-----KARGAVLEKTLGYNIMYPPESN-TNL---TETMTNTNOOLELHGG 295
DB 661 LMKPLTKNDLSQSVRRYVVKHRTAHNGWSEDEVGRNTLTLFMTPEPAHT----- 709
OY 296 ESFWWSMISYNSLGSVP-----ATLRIPALQEKSFQIEVMAQVADOLVYKWS 347
DB 710 ---VTVLAVNSLGSILVNFNLTFSPMKSVAVE--SLSAVPLSSSCV-----ILSWTL 758
OY 348 SALDVNT--WMIEWPDDVSEPTLWESVSQATNWTIQODKLPFCWYNISVYPLMDK 405
DB 759 SPDDISLYLVIEW--KLINEDGKKWLRIPSNVAKKFIHDFTPIEKYQESLYVVEEG 816
OY 406 VGEPSIOAYAKEGVSEGPETKVENIGVTVTITKEIPKSEKGIICNTIITYOAEQGG 465
DB 817 VGRPKILNGFTRDAIDKQ-----QNDAG 839
OY 466 KGFSTVNSIIQYGLSKRKRTSYVOVMASTASAGTNGTSINFKTLSPSVFELLITLS 525
DB 840 L-----YVIPI 846
OY 526 LIGGGLLILITVAYGLKKPNKLTFLCPTVPNPASSIATWHDGDFKDLMLKE 581
DB 847 IISCVLLGLTILLISH-----QRMKKLFWDDVPNPKNCSSWA--QLNFKQDISLHE 895

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Search completed: August 4, 2003, 11:26:06
 Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:17:11 ; Search time 26 Seconds
(without alignments)
1323.983 Million cell updates/sec

Title: US-09-892-949-2
Perfect score: 3908
Sequence: 1 MMTWALMMLPSLCKFSLAA.....VTAREFLVSEKLPENTKGEV 732

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688.5	17.6	917	116B_MOUSE	Q00560 mus musculus
2	682.5	17.5	918	116B_RAT	P40190 rattus norv
3	679.5	17.4	918	116B_HUMAN	P40189 homo sapien
4	517.5	13.2	836	116B_HUMAN	Q09062 homo sapien
5	471.5	12.1	837	116B_MOUSE	P40223 mus musculus
6	408.5	10.5	1097	116B_HUMAN	P42702 homo sapien
7	405.5	10.4	1092	116B_MOUSE	P42703 mus musculus
8	385	9.9	874	112S_MOUSE	P97378 mus musculus
9	383	9.8	874	112S_MOUSE	Q09665 homo sapien
10	242.5	6.2	1162	112R_MOUSE	Q62959 rattus norv
11	231.5	5.9	662	112R_MOUSE	P43701 homo sapien
12	227	5.8	662	112R_MOUSE	P43356 mus musculus
13	226	5.8	738	112R_MOUSE	Q06837 mus musculus
14	224	5.7	3119	112R_MOUSE	Q06847 mus musculus
15	221	5.7	1165	116B_HUMAN	P46357 homo sapien
16	219.5	5.6	830	116B_HUMAN	Q09374 columba liv
17	208.5	5.3	831	116B_HUMAN	Q08235 cervus elap
18	205	5.2	831	116B_HUMAN	Q04594 gallus gall
19	204	5.2	1165	116B_MOUSE	Q02671 sus scrofa
20	201	5.1	831	116B_MOUSE	Q09104 meleagris g
21	200	5.1	1163	116B_MOUSE	Q09104 meleagris g
22	198.5	5.1	610	116B_MOUSE	P05710 rattus norv
23	191	4.9	608	116B_MOUSE	Q08501 mus musculus
24	189	4.8	581	116B_MOUSE	Q04561 ovis aries
25	188	4.8	639	116B_MOUSE	Q02992 oryctolagus
26	187.5	4.8	581	116B_MOUSE	Q02172 bos taurus
27	185	4.7	3063	116B_MOUSE	Q099715 homo sapien
28	182.5	4.7	1897	116B_MOUSE	P10588 homo sapien
29	176.5	4.5	1912	116B_MOUSE	P23468 homo sapien
30	175.5	4.5	2481	116B_MOUSE	Q091740 xenopus lae
31	171	4.4	1447	116B_MOUSE	P43146 homo sapien
32	169.5	4.3	2386	116B_MOUSE	P10751 homo sapien
33	169	4.3	616	116B_MOUSE	P14787 oryctolagus

34	169	4.3	929	1	CA1C_NOTVI	Q01145 notophthalm
35	168	4.3	1238	1	PRPJ_MOUSE	Q04455 mus musculus
36	168	4.3	2029	1	LAR_DROME	P16621 drosophila
37	166	4.2	1447	1	DCC_MOUSE	P70211 mus musculus
38	163.5	4.2	1461	1	NEOL_HUMAN	Q02859 homo sapien
39	162.5	4.2	1377	1	NEOL_RAT	P97603 rattus norv
40	161.5	4.1	2012	1	DECA_HUMAN	Q04669 homo sapien
41	160.5	4.1	2201	1	TENA_HUMAN	P24821 homo sapien
42	159	4.1	2200	1	LAR_CAEEL	Q09008 caenorhabdi
43	158.5	4.1	1328	1	FINC_PLEMA	Q01289 pleurodeles
44	158.5	4.1	2265	1	FINC_BOVIN	P07589 bos taurus
45	158	4.0	424	1	1131_MOUSE	Q09030 mus musculus

ALIGNMENTS

RESULT 1
ID IL6B_MOUSE STANDARD: PRJ: 917 AA.
AC Q00560:
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN IL6ST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibi M., Tega T., Kishimoto T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal
RT transducer, gp130, and its regulated expression in vivo.";
RT J. Immunol. 148:4066-4071(1992).
RL J. Immunol. 148:4066-4071(1992).
CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, IL-6, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT.
CC - SUBUNIT: Heterodimer of an alpha and a beta chain.
CC - TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
CC EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
CC CELLS.
CC - DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
CC DURING THE REST OF EMBRYOGENESIS.
CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC - SIMILARITY: Contains 5 fibronectin type III domains.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X62646; AAA44515.1; -
CC EMBL: M83336; AAA37723.1; -
CC PIR: I49699; I49699.
CC HSSP: P40189; 1B0U.
CC MGD: MGI:96560; 116st.
CC GO: GO:0007165; P:signal transduction; IDA.
CC Interpro: IPR002996; CRIA.

DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 5.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 KW Repeat.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).
 FT TRASMEM 618 639 POTENTIAL.
 FT DOMAIN 640 917 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 120 IG-LIKE C2-TYPE.
 FT DOMAIN 124 220 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 221 322 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 323 420 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 422 515 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 516 611 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 723 741 SER-RICH.
 FT DISULFID 28 54 By similarity.
 FT DISULFID 48 103 By similarity.
 FT DISULFID 134 144 By similarity.
 FT DISULFID 172 180 By similarity.
 FT DISULFID 426 464 By similarity.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 917 AA; 102452 MM; PCEPD20HC2466f4 CRC64;

Query Match 17.6%; Score 688.5; DB 1; Length 917;
 Best Local Similarity 26.5%; Pred. No. 1.6e-44;
 Matches 204; Conservative 130; Mismatches 317; Indels 119; Gaps 24;

22 PAKPENISGVYVYRNLTCTMSPKETSX-TOYTVKRYVAGEGKNDCTNSTSENAS 80
 126 PDKPTNLCTIVNEGKMLCQMDPGRETYLETWTYTKSEMA-TEKPPDOCKHGT-----S 179
 81 CSF-FLPRITTPDNTYIEVEANGGVKSHMTYVRLNIAKTEPKIFRYKPVLGIRK 139
 180 CMVSTMPPTYV--NIEVWVEAENALGVKSESINFDPAVKVPTPPYMLSTNSELSSI 237
 140 IQIEIKPELAPVSSDLTYTLAFTVNSTSMVEVFAANRDKNTYMLTGQPTTEYVI 199
 238 LKLSWVSSGLGL-LDLKSDIOYRKDASTWIOVPL-EDTMSPTSTFVODLKPTTEYVF 295
 200 ALRCVAKES--KFWSDMSQEKMGMTTEEAPC-GLELMVHLKPAEADGRRPVLLKKARG 256
 296 RIR-SIKSGKGYWDMSEELASGTYEDRPSRPSFWKTNPSHQEKRVRALLIKALPL 354
 257 APVLEKTLGVNIWYIPESNTNLTETMNTTNOQLHLHGEGSEFWSMISYLSGKSPVATL 316
 355 SEANGLIDYEV--ILTQSKSVSQTYVTGTELVNLINDRYVASTVLAARNVKGSAAVL 412
 317 RIPAPQEKSFQCIEMQACVAEDOLVVKWSSALDVNTWMLTEMFDPDVUSEPTTLSEVVS 376
 413 TTPSPHTVAAYSVNLKAFPKDNLMLWEMTPPPKVSAYIIEWCVLSENACVDEMOED 472
 377 QATWNTIQODKLKPEWCYNISVYPLHDKVGEPPYSIOAYAKGVSEPEPTKVENIGYKT 436
 473 ATVNTHTLRGLRLEKCYQITVTFYFATGPGSESLKAYLKQADAPARPTVATKTKVGVNE 532
 437 VTIWKEIKSEKRGKIIICNYTIFYQAEKGKFSKTVNSIIQYGLSLKRTSYIVQYMA 496
 533 AVLAMDQIPVDVDMGFIINYSISYTSYKEMVAVHDSHTEYTLSSLDPLVVRMAA 592
 497 STSAGGTGTSINFTLSFSVEIILITSLGGGILLIILTVAYGLKPKKLHLCPPT 556

DB 593 YTDEGKDGDEPFTFTTPKFAQGEIATVPCVLAFLITLLGLVLCFCKNRDLKKHIWPN 652
 QY 557 VNPAPASSIATW-----HGDPFKDKLNKESDSS-----VNTEDILKPCSTPSOKL 603
 DB 653 VPDPKSHIAQWSPHTPPRHNFNSKDM---YSDGNFTDVSVETEANNKRPC--PDOLK 707
 QY 604 VIDKLAVNFGVNLQEIFTDE--ARTGOENILCG----- 634
 DB 708 SVD-----LFFKEKYSTEGHSGGICGSSCMSSSRPSISSNEENSAOSTASTV 755
 QY 635 EKNGVTCPPRPDCLGKSF-----EELPV-----SPEIPRKSOYLK 672
 DB 756 EKFSTVHSHGYRQVPSVQVFSRSESTOPLDSEEPEDLQIADVSDGDELLPRQPYKQ 815
 QY 673 S-----RMDEGTPREAKCOLLEFG-----GSLVDPDICEBAPPY 708
 DB 816 NCSQPEACPEISHFRSMQVL-SGNEEDPVRLKQOOVSDHLSQ-----PY 859
 RESULT 2
 IL6B_RAT
 ID IL6B_RAT STANDARD: PRT: 918 AA.
 AC P40190;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin 6 signal transducer) (Membrane glycoprotein 130) (GP130).
 GN IL6ST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93052397; PubMed=1427893;
 RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
 RT "Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule, gp130."
 RL Genomics 14:666-672(1992).
 CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES. AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC - SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC - TISSUE SPECIFICITY: Type I membrane protein.
 CC - TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS AND ENDOTHELIAL CELLS.
 CC - SIMILARITY: Contains 5 fibronectin type III domains.
 CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).
 CC CC
 CC EMBL: M92340; -; NOT_ANNOTATED_CDS.
 DR PIR: A44257; A44257.
 DR HSSP: P40189; 1B0U.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 4.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;

```

KW Repeat. 1 22 POTENTIAL.
FT SIGNAL 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT CHAIN 23 618 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 619 640 POTENTIAL.
FT TRANSMEM 641 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE.
FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.
FT DOMAIN 222 323 FIBRONECTIN TYPE-III 2.
FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.
FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.
FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.
FT DOMAIN 724 754 SER-RICH.
FT DISULFID 28 54 By similarity.
FT DISULFID 48 103 By similarity.
FT DISULFID 134 144 By similarity.
FT DISULFID 172 181 By similarity.
FT DISULFID 457 465 By similarity.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 918 AA; 102450 MW; 9E18B6FEFCF087F7 CRC64;

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Query Match 17.5%; Score 682.5; DB 1; Length 918;
Best Local Similarity 27.0%; Pred. No. 4.5e-44;

Matches 214; Conservative 125; Mismatches 339; Indels 115; Gaps 25;

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OY 22 PAKENISCVYVYRNKLTCTWSPEKETS-TOYVRYRYAEGEKHNDCTNSSTSENKAS 80
DB 126 PDIPNTNISCIVNEGKMLCQDPRGRETLETNYTLKSSMA-TEKPPDCRTKHGTS-SS 180
OY 81 CSF-FLPRTIPDNTTIVEANGDGVKSHMTYRLNLEAKTEPKLFRKYPVIGIRRM 139
DB 181 CMGCTPIYFV--NLEVVVEAEMALGNVSSSEPIINDPVKPKSPPHNLSTYNSSELSI 238
OY 140 IOEIMKPELAPVSSDLKYTLRFTVNSTSMMEVFAKNRKDKNOTYMLTGLOPTEVVI 199
DB 239 LKLANVNSGLDSILR-LKSDIOYRKDKASTNIQVPL-EDYSPRSFIVODLKPTTEVVF 296
OY 200 ALRCAYKES--KFSWDSQOEKMGMTTEBAPC-GELMRYLKPAAEDGRRPVALLMKKARG 256
DB 297 RIR-SIKENKGGYMSDEEASGTYEDRPSKAPSFYKVNANHPQEVRSARLIMKTLPL 355
OY 257 APVLEKTLGYNIWYPPESNTNITEMNTNOOLEHLOGESFVWSMISYNSIGKSPVATL 316
DB 356 SEANKKILDYEVVLTKSSVSQTYVNGT--ELVNLNNRVASLALARNVYKSPAYVL 413
OY 317 RIPAIQESFOCIEVMAQVAEDOLVVKMOSSALDVNTMIEMFADVSEPTTLESWSVS 376
DB 414 TTPGSHFASHHPVDLKAFPKDNLLVEMTPSPKVVNKTILEMCVLSSENSPCIPWQOED 473
OY 377 QATMWTIOQDKLKPEWKNISVYPMILHDVGEPEYSIOAYAREGVSSEPTKVENIGVKT 436
DB 474 GTVNTHLRGLSLLESKYLLITVYFPGPGSPSPESMKAYILQAAARSKGPTVATKVGNE 533
OY 437 VTITWKEIPKSEKCIITNYITFYQAEKGKFSKTVNSIIQYGLSILKRTSYIVQMA 496
DB 534 AVLEMDHLDPVVOQNFIRNYSISYRTSVGKEVNVVDSHREYTLSSISDPLVYVHMA 593
OY 497 STSAGTGTSTINFKTISFVFEIITLSLGGGLLILITVAAGLKKPKNLTHICMPT 556
DB 594 YTEBGKRGKGPETFTTLKFAQGEIAYVPCALATLITLGLVLCFCFKRDLIKHINPN 653
OY 557 VPNAESSIATW-----HGDDFKDKL-NLKESDGS-VNTEDRILKPCSTPSDKLVID 606

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DB 654 VPDPKSHIAQMSDPTTPRHNFNSKQMYSDANFTDVSVEIEANKKPC--PDDLKSLD 711
OY 607 KLVNFGVNOIEITLDE--ARTGOENNLGG-----EKN----- 637
DB 712 -----LFEKKEISTEGHSGIGGSSCMSSSRPSSISSSENSAOSTASTVOYS 759
OY 638 GYVTCPPRPDPCPLGKSF-----EELP-----VSEIIPKRSOYLRSRM 675
DB 760 TVVSHGTRHQVPSVOVFSRSESTQPLDSEERPEDLQVDSGDELIPKQOYTFKQSCS 819
OY 676 PEGTRPE-----AKEDLLFSGQSLVPHDLCEGAPNPYLKNSVTAREF---L 719
DB 820 QPGASPDVSHFRGSSQVPSGSEDEPVRLLKQOVSDFHISE-----PY--GSGORRLFCQGS 872
OY 720 VSEKIPERTKGEV 732
DB 873 VADALGTGTGDOI 885

RESULT 3
IL6B_HUMAN STANDARD: PRT: 918 AA.
AC P40189; Q90041;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (Gp130) (Oncostatin M
DE receptor) (CDW130) (CD130 antigen).
GN IL6ST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637;
RA Hibb M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RL Cell 63:1149-1157(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Synovium;
RX MEDLINE=20341529; PubMed=10880057;
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RX Murakami M., Nakao K.;
RT "Cloning of novel soluble gp130 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis."
RL J. Clin. Invest. 106:137-144(2000).
RN [3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21269388; PubMed=11098061;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT "Determination of the disulfide structure and N-glycosylation sites of
RT the extracellular domain of the human signal transducer gp130."
RL J. Biol. Chem. 276:8244-8253(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE=98169383; PubMed=9501088;
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130."
RL EMBO J. 17:1665-1674(1998).
CC -I- FUNCTION: Signal-transducing molecule. The receptor systems for
CC IL-6, LIF, OSM, CNTF, IL-11 and CT-1 can utilize gp130 for
CC initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)
CC complex, resulting in the formation of high-affinity IL-6 binding
CC sites, and transduces the signal. Does not bind IL-6. May have a
CC role in embryonic development (By similarity).
CC -I- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC secreted (isoform 2).

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CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P40189-1; Sequence=Displayed;
CC Name=2; Synonyms=GPI30-RAPs;
CC IsoId=P40189-2; Sequence=WSP_001684, WSP_001685;
CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines
CC examined. Expression not restricted to IL-6 responsive cells.
CC -1- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
CC (RA) but it is not specific to patients with RA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M57230; AA559155.1; -
DR EMBL: AB015706; BAA78112.1; -
DR PIR: A36337; A36337.
DR PDB: 1B0U; 26-AUG-98.
DR PDB: 1B38; 13-JAN-99.
DR PDB: 11IR; 28-MAR-01.
DR Genew: HGNC:6021; IL6ST.
DR MIM: 600694; -
DR GO: GO:0005887; C:integral to plasma membrane; TAS.
DR GO: GO:0004898; F:gpl30; TAS.
DR GO: GO:0004924; F:oncostatin-M receptor activity; TAS.
DR GO: GO:0004872; F:receptor activity; TAS.
DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hemtopoptn_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS01533; HEMATOPO_REC_L_F2; 1.
DR Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat; 3d-structure; Alternative splicing.
FT SIGNAL 1 22
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 620 641 POTENTIAL.
FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 124 120 IG-LIKE C2-TYPE.
FT DOMAIN 223 222 FIBRONECTIN TYPE-III 1.
FT DOMAIN 325 324 FIBRONECTIN TYPE-III 2.
FT DOMAIN 424 517 FIBRONECTIN TYPE-III 3.
FT DOMAIN 518 613 FIBRONECTIN TYPE-III 4.
FT DOMAIN 725 755 FIBRONECTIN TYPE-III 5.
FT DISULFID 28 54 SER-RICH.
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 182
FT DISULFID 458 466
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .).
FT VARSPLIC 325 329 RPSKA -> NIASF (in isoform 2).
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FT VARSPLIC 330 918 /FTID-VSP_001684.
FT STRAND 130 137 Missing (in isoform 2).
FT TURN 138 139 /FTID-VSP_001685.
FT STRAND 143 147
FT STRAND 157 164
FT TURN 165 166
FT STRAND 167 168
FT STRAND 172 173
FT TURN 179 180
FT STRAND 181 183
FT TURN 190 191
FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 208
FT STRAND 212 214
FT HELIX 216 218
FT STRAND 220 221
FT STRAND 226 231
FT STRAND 240 245
FT HELIX 248 251
FT TURN 252 252
FT STRAND 255 263
FT TURN 264 265
FT STRAND 270 271
FT HELIX 274 277
FT STRAND 283 286
FT STRAND 293 303
FT TURN 304 305
FT STRAND 317 321
FT HELIX 325 331
SQ SEQUENCE 918 AA; 103522 MW; D813F3672D010D53 CRC64;

Query Match 17.4%; Score 679.5; DB 1; Length 918;
Best Local Similarity 28.4%; Pred. No. 7.7e-44;
Matches 175; Conservatve 113; Mismatches 261; Indels 67; Gaps 16;

22 PAKPENISCVYYRRNLCTWSPGKETSY-TOYTVK---RNYAFGE---KHD---NCTTN 71
126 PEKPNLSCIVNEGKKMKCEMDGGRHLEHLENTFKSEMAHKHPADCAKRDTPICVVD 185
72 SSTSERNRASCFFELPRITIPDNYTIEVEAENGDVYKS-HMTYRLENIARTPEPKIRY 130
186 YST-----YEFV-----NIEVVAEAEALGKVTSDHINFDVYKV-KPNPNNLSV 230
131 KPVLGIRKMIQIEMIKPELAPVSSDKTTLFRFVYNSISMEAEVNAKRRKKNQTYNLTG 190
231 INSEELSSILKRLWTNPISIKSVTI-LKYNIOYRTKADASTWSQIP-PEDTASTRSSFFVQD 288
191 LOPFEVYIALRCAYKESK-FMSDMOSEKMGMTTEAEAPC-GLELWRVLKPAEADGRPRVR 248
289 LKPFIEYVFRIRCKMEDKDGYSWDSSEASGITTYDRSKAPSFYKIDPSHTQGYRIVQ 348
249 LLMKRGAPVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLCGESFVWSMISYNSL 308
349 LVMKTLPPFEANGKILIDYEVTILTRKSHIQNTVNAI--KLTVINLTNDRYLATILVRMLV 406
309 GKSPATILRIPALIQKSSQCIENVMOACVAEQOLVYKMQSSALDVNTWMIENFPPVDSPT 368
407 GKSDAAVLTIPACDFQATHPVMDKAPFKDMKLWEMTTPRESVAKKYLLEKCVLSDKAPC 466
369 TLSMESVSQATNMTTIOQOKLKEPFCYNISVYPMILDKVGEPSIOAVAKEGVSPSEPTK 428
467 ITDMQDEGTYHRTILRNLNLESKCYLITVPVYADGSGSPESIKAYIKQAPPSKGPVVR 526
429 VENIGVKTVTITWKEIPKSEKGIICNTIFYOAGGKGFSTYNSILOYGLESLKRT 488
527 TKVQKNDAVLEMDQLPDVQNGFIRNTYIFRTIIGNETAVNVDSSHTETLSLSDT 586
489 SYIYOVMASTAGGNGISINFKTLSEVFELLITLSLGGGLLILITLYAVYGLKRNK 548
587 LYWRMAAYVTDEGGKDGPEFTTTPKFAQGEIEAIVPVCIAFLITLLGLVLCFENKRD 646
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RX MEDLINE=97331327; PubMed=9187659;
 RA Yamaeaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
 RT "solution structure of an extracellular domain containing the WsXWS
 RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand";
 RL Struct. Biol. 4:498-504(1997).
 CC - FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 CC ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 CC THE CELL SURFACE.
 CC - SUBUNIT: DIMER (PROBABLE).
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC - SIMILARITY: Contains 5 fibronectin type III domains.
 CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M58288; AAA37673.1; -
 CC PIR: A34898; A34898.
 CC DR PDB: 1GCF: 22-OCT-97.
 CC DR PDB: 1CNO: 22-OCT-97.
 CC DR PDB: 1GDS: 08-MAR-00.
 CC DR PDB: 1GGR: 08-MAR-00.
 CC DR MGD: MGI:1339755; Csf3r.
 CC DR GO: GO:0030593; P:neutrophil chemotaxis; IMP.
 CC DR InterPro: IPR002996; CRIA.
 CC DR InterPro: IPR003961; FN_III.
 CC DR InterPro: IPR003529; Hemtopoptn_L_F2.
 CC DR Pfam: PF00041; fn3; 3.
 CC DR SMART: SM00060; FN3; 2.
 CC DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 CC KM Cell adhesion: Receptor; Repeat: Signal; Transmembrane;
 CC Immunoglobulin domain: Glycoprotein; 3D-structure.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 837
 CC FT DOMAIN 26 626
 CC FT TRANSSEM 627 650
 CC FT DOMAIN 651 837
 CC FT DOMAIN 118 118
 CC FT DOMAIN 122 228
 CC FT DOMAIN 229 333
 CC FT DOMAIN 334 431
 CC FT DOMAIN 432 528
 CC FT DOMAIN 529 624
 CC FT DISULFID 132 143
 CC FT DISULFID 249 296
 CC FT DISULFID 267 310
 CC FT CARBOHYD 51 94
 CC FT CARBOHYD 129 129
 CC FT CARBOHYD 186 186
 CC FT CARBOHYD 279 279
 CC FT CARBOHYD 392 392
 CC FT CARBOHYD 408 408
 CC FT CARBOHYD 474 474
 CC FT CARBOHYD 487 487
 CC FT CARBOHYD 582 582
 CC FT CARBOHYD 613 613
 CC FT CARBOHYD 232 235
 CC FT CARBOHYD 249 255
 CC FT STRAND 266 274
 CC FT STRAND 281 286
 CC FT STRAND 290 296
 CC FT STRAND 303 311
 CC FT STRAND 323 328

SQ SEQUENCE 837 AA: 93406 MW: 422959892C8531 CRC64;
 Query Match 12.1%; Score 471.5; DB 1; Length 837;
 Best Local Similarity 25.38; Pred. No. 5.3e-28;
 Matches 185; Conservative 105; Mismatches 293; Indels 147; Gaps 33;
 QY 22 PAKPENISCVYYRRKN-LTCTWSPGKETSY-TQYTVRYTAFGEKHNDCTNST----- 74
 DB 124 PAPSRLNLSCLMHLTNSLVCQWBERPETHLPTEFIILK-----SFRSRAD-CQYQGDITPDVC 179
 QY 75 -SENRAISCFELPRITIPDNYTIEVEANGDGYIKSMYTRLENIKTEPKI--FRVK 131
 DB 180 AKRKQNNCSIPRKNLLLYQYMAIWOQENMLGSESPKLCDDPDVYKLEPPMIALDLTG 239
 QY 132 PVL-----GIKRMQIEMIRPELAPVSSDLKYLRFTVSTSMMEVFKKNDKQTY 166
 DB 240 PDVAVSHQPGCLMWSKRWKPEYWEDECELRYPOLKGAN--WTLVFHLPSKDD--F 293
 QY 187 NLNGLOPTEFYVALRCVAKES--KFWSDMSQEMKWTDEAP-CGLELRVLPAPADG 243
 DB 294 ELGGLHAPRYTTLQMR-IRSSLPGFSPSPGLQLRPYKAPTIIRLDTCQCKOLD-PG 351
 QY 244 RRPVRLMKRKARCAPVLE--KTLGYNI-WYPESSNTLLETMTTNOQLHLGSEFW 299
 DB 352 TVSVQLFWRP---TPLOEDSGQIOGYLLSNWSPDHQODIHLNNTQQLSCIFLLPSEAQN 408
 QY 300 VSMISYNSLSKSPATIRIRAIQESKFCQIEVWQACVAEQOLYVKKQSSALDVNTMIEM 359
 DB 409 VTLVAVYKAGTSSPTTY--VFLEN-----EGPAVTGLIAMAQDINTJTWVDW 452
 QY 360 -FPDVDEPTTLTWSVSQATN-----WTIQ-----ODKLKPFMCYNISVYPMH 403
 DB 453 EASSLPQGLIEMKSPSPYNNYSKSMLEPNONITGILLKONINFOLYRITVADLP 512
 QY 404 DKVGEPISTAVAKGVSPGSEPTKVENIGVKTIVTWKIEPKSERKGI--CNVYTFYQ 461
 DB 513 GIYGPVAVYTFGERAPRPHAPALHLKIVGTWMAQLEW--VPEAPRLGMIPLNHYTFWA 570
 QY 462 AEGGKGSKIVNSSLIOGLSEIKRKTSTYVOWASTSAGTNGTSINFTLSFSVREI 521
 DB 571 DAGHSSVTLNISTLHDFVTLKLEPASYLVHVAITSRASTNGTGLTFLPDSLNTF 630
 QY 522 LITSLIGGLIILITLVAAGLKKPKNLTHLC-----WPPVPAARSSTIATGDD 572
 DB 631 L-----GLTCLVLSTTC-----VTMLCCRRKRTKSTFMSVPPRAISSLSWL--- 674
 QY 573 FKDKLNKESDVSNTEDRIKPCSTPSDKLVYDKLVVNGVNLQELFTDEARTGOENL 632
 DB 675 -----PRIMTEETQLPSFMSVPSITKIN-----ELEEDKKPTHMDSSES 715
 QY 633 GGEKNGVTC-----PFRP-DCPLKSPFELPVSEIIPPKSQYL 671
 DB 716 SG--NGSLPALVQAYVLQGPREISNOSOPPSRTGQVLYGQVLESPTSQGV---MOYI 769
 QY 672 RSSRAPESTRP 681
 DB 770 RS---DSTOP 776
 RESULT 6
 LIFR_HUMAN STANDARD; PRT: 1097 AA.
 ID LIFR_HUMAN PA2702;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leukemia inhibitory factor receptor precursor (LIF-R).
 GN LIFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Placenta;
 RX MEDLINE-92007727: PubMed-1915266;
 RA Geating D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,
 RA King J., Price V., Cosman D., Beckmann M.P.,
 RT Leukemia Inhibitory factor receptor is structurally related to the
 RT IL-6 signal transducer, gp130.";
 RL EMBL J. 10:2839-2848(1991).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
 CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
 CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
 CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
 CC MEMBRANE-BOUND AND A SECRETED FORM.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms-2;
 CC Name-1: Synonyms-Membrane;
 CC IsoId-P42702-1; Sequence-Displayed;
 CC Name-2: Synonyms-Secreted;
 CC IsoId-P42702-2; Sequence-Not described;
 CC Note-No experimental confirmation available;
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: X61615; CAA43805.1; -
 DR PIR: S17308; S17308.
 DR Gene: HGNC:6597; LIFR.
 DR MIM: 151443;
 DR GO: GO:0005887; C: Integral to plasma membrane; TAS.
 DR GO: GO:0004923; F: Leukemia inhibitory factor receptor activity; TAS.
 DR GO: GO:0007166; F: cell surface receptor linked signal transdu. . . ; TAS.
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 5.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 DR Receptor: Transmembrane; Glycoprotein; signal; Alternative splicing:
 KW Repeat.
 FT SIGNAL 1 44
 FT CHAIN 45 1097
 FT DOMAIN 45 833
 FT TRANSMEM 834 858
 FT DISULFID 859 1097
 FT CARBOHYD 55 65
 FT CARBOHYD 64 64
 FT CARBOHYD 85 85
 FT CARBOHYD 131 131
 FT CARBOHYD 143 143
 FT CARBOHYD 191 191
 FT CARBOHYD 243 243
 FT CARBOHYD 303 303
 FT CARBOHYD 390 390
 FT CARBOHYD 407 407
 FT CARBOHYD 426 426
 FT CARBOHYD 445 445
 FT CARBOHYD 481 481
 FT CARBOHYD 489 489
 FT CARBOHYD 572 572
 FT CARBOHYD 652 652
 FT CARBOHYD 663 663
 FT CARBOHYD 680 680
 FT CARBOHYD 729 729
 FT CARBOHYD 787 787
 FT CARBOHYD 1097 787
 FT AA: 123742 MW: C8602897E359FCES CRC64;
 FT SEQUENCE

Query Match 10.5%; Score 408.5; DB 1; Length 1097;
 Best Local Similarity 21.3%; Pred. NO. 5.2e-23;
 Matches 178; Conservative 139; Mismatches 292; Indels 225; Gaps 40;
 Db 22 PAKENISCVYYRNKILCTWSPKERTSY-----TOYVTKRTVAFGKHDCNTNSSTSE 76
 Db 333 PDLTQQLNCETHDLCIKESNNPGRVIALVGPRTASTLVESFS-GKVRILKRAEAPLTNE 391
 Db 77 NRACSFPLPILTPDNTTIVEAENGDVTKSMYTRLENLA-KIEP-PKIFKAPV 133
 Db 392 SYQLLFQMLPQOEI--YNFTLNANPLG--RSOSTI--LVNITEKYVPHPTSFKYVDI 444
 Db 134 LGIKRMIOIEWIKPELAPVSSDLKYTLREFTVNTSMWEV--NEAKNRK-----KNQ 184
 Db 445 --NSTAVKLSMHLG-----NFAKINFLCELEIKSKSVQDQRVNTTKGVENS 490
 Db 185 TY--NLGLQFTEVYIALRCVAKESKFSWDSQEKMGMEELAPC-GLEMLRVLPAPAA 241
 Db 491 SYVALDKLNPITYLTFIRICSTEFEMKSKMKKHILTEASPSKGPDTM--EWS 547
 Db 242 DGRPRVLLMKKAGAPVLE--KTLGYNWYEPESNTNLTETMTNTOQLHLGGESEF 298
 Db 548 DGNMLI-LYMRP---LPINEANGKILSYNVCSSDEETQSLEIPDQHKREIRLDKNDY 603
 Db 299 WSMISYVSLGKSP---VATLRIPALDEKSPQIEVMQACVAEDQLVVQMOSALDVNTW 355
 Db 604 IISVYANKSVSSPSPKASKSEIRNDLKIQVYMGKG-----ILLTHYDPNMTCDY 657
 Db 356 MIEFPPDVSEPTLWSV--SOATNMNTQDCLKPWCYNISV-----YPMHLKVG 407
 Db 658 VIKKNSRSRSPCLMDMKKVPNSSTERYIESDERPRGIRNFFLYGCRNGYQLLRSMIG 717
 Db 408 EPTYSQVYAKGVSEGEPTFVENIGKVTYITTKELPKSKRKIIICNTITFYAEGCKG 467
 Db 718 -----YIEELAPVAPNFTVEDTSADSLVKKMEDIPVEIRLFGYLFYF---GKG 766
 Db 468 FSKTVNSIIQYG-----LESILKRTSYIVQVMASTSGTNGTSIN 509
 Db 767 EROTSKMRVLESGSDIKVKNITDISOKTLRIADLOKTSYHLVLRAYTGGVPEKSMY 826
 Db 510 FKTLSEVFEIILITSLGGGLLILITVAYGL-----KKPNKLTHLCWPTVP 558
 Db 827 VVTKENSV-----GLITAILPVAVAIVGVVTSILCYRRREWMKETFFYPIDP 874
 Db 559 NPASSTATWGDGDFKXKLNKESDQSVNEDRLKPCSPDGLVID----- 606
 Db 875 NPENCKALQF-----QKSYCEGSSALKTLE--MNPQ-TPNNVEVLETSAPKIEDTE 924
 Db 607 -----KLNVNF-----GNVLOEIFPD----- 622
 Db 925 IISVAPRPEDRSADPEENHVVSYPPIIEEIPNPAADAGTAQVIYIDVGSYMQPQ 984
 Db 623 -EARTGEBNN-LGGEKNGVYTCPPRPD--CPLGKSEFELVSPPIPPRKSOYLRSRMEG 678
 Db 985 AKPEEEDNPEDVAGGA--GY-----KPMHLPINSTVEDIAAEELD-----KTAG 1027
 Db 679 TRPAKQQLLEFSGSLVPD-----HLCEBAPNPYLKNSVTAREFLVSEK 723
 Db 1028 YRPQAN--VNTMNLVSPDSPRSIDNSSEIVSFSP-----CSINSKQPLIPPK 1073
 RESULT 7
 LIFR_MOUSE
 ID LIFR_MOUSE STANDARD: PRT: 1092 AA.
 AC P42703;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Leukemia inhibitory factor receptor precursor (LIF-R) (D-factor/LIF
 DE receptor).
 GN LIFR.
 OS Mus musculus (Mouse).

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 2).
RX	MEDLINE=92007727; PubMed=1915266;
RA	Gearing D.P., Thut C.J., Vandenbos T., Gimpe S.D., Delaney P.B.,
RA	King J., Price V., Cosman D., Beckmann M.P.;
RT	"Leukemia inhibitory factor receptor is structurally related to the
RT	IL-6 signal transducer, gp130.";
RL	EMBO J. 10:2839-2848(1991).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORM 2).
RC	STRAIN=ICR; TISSUE=Liver;
RX	MEDLINE=94039833; PubMed=7901054;
RA	Tonida M., Yamamoto-Yamaguchi Y., Hozumi M.;
RT	"Pregnancy associated increase in mRNA for soluble D-factor/LIF
RT	receptor in mouse liver.";
RL	FEBS Lett. 334:193-197(1993).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX	MEDLINE=94334302; PubMed=8056772;
RA	Tonida M., Yamamoto-Yamaguchi Y., Hozumi M.;
RT	"Three different cDNAs encoding mouse D-factor/LIF receptor.";
RL	J. Biochem. 115:557-562(1994).
CC	-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
CC	WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
CC	LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC	-1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
CC	MEMBRANE-BOUND AND A SECRETED FORM.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=1; Synonyms=Membrane;
CC	Isoid=P42703-1; Sequence=Displayed;
CC	Name=2; Synonyms=Secreted;
CC	Isoid=P42703-2; Sequence=VSP_001686, VSP_001687;
CC	Note=No experimental confirmation available;
CC	-1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN,
CC	AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF THE
CC	SECRETED FORM.
CC	-1- SIMILARITY: Contains 4 fibronectin type III domains.
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC	-----
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CC	-----
DR	EMBL: S73496; AAC60698.1; -;
DR	EMBL: S73495; AAC60697.1; -;
DR	EMBL: D26177; BAA05165.1; -;
DR	EMBL: D17444; BAA04258.1; -;
DR	PIR: JX0312; JX0312.
DR	MGD: MGI:96788; L1fr.
DR	InterPro: IPR002996; CRLA.
DR	InterPro: IPR003961; FN.III.
DR	InterPro: IPR003529; Hemtopoptn_L_F2.
DR	Pfam: PF00041; FN3; 4.
DR	SMART: SMO0060; FN3; 4.
DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW	Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
KW	Repeat.
FT	SIGNAL 1 43
FT	CHAIN 44 1092
FT	DOMAIN 44 828
FT	TRANSMEM 829 853
FT	DOMAIN 854 1092
FT	DISULFID 53 63
FT	CARBOHYD 164 164
FT	POTENTIAL.
FT	LEUKEMIA INHIBITORY FACTOR RECEPTOR.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	BY SIMILARITY.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHD	199	199	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	238	238	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	261	261	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	385	385	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	402	402	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	421	421	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	440	440	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	453	453	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	476	476	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	567	567	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	647	647	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	658	658	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	675	675	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	724	724	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHD	782	782	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	VARSPLIC	718	719	AP -> EA (in isoform 2).	
FT				/FTId-VSP_001686.	
FT	VARSPLIC	720	1092	Missing (in isoform 2).	
FT				/FTId-VSP_001687.	
SEQ	SEQUENCE	1092 AA;	122573 MW;	6F02BBC8E15ADE70 CRC64;	
Query Match		10.4%;	Score 405.5;	DB 1;	Length 1092;
Best Local Similarity		21.7%;	Pred. No. 8.8e-23;		
Matches	180;	Conservative 131;	Mismatches 304;	Indels 213;	Gaps 36;
OY	22	PAKBNISCVYVYRRNLCTWSPGKENSYS	-----TQYTV-----	-----KRT	58
Db	328	PDVQPKLSCEHDLKEIKCSMNPGRITGLVGRPNTEYTLFESISGSKAVPRIEGTLNET			387
OY	59	YAFG-EKHDCNTWSSISENRSASFELRLTIPDNTYIEVANGDGVIKSHMTWBLE			117
Db	388	YRLGQMHGPGQEHNFLLTGR-----	-----NPLQAOASAVAVINTE		424
OY	118	NIATTEPKIRRVVPLGIKRMIOLEWIKPELAPVSDLKATLRLRPVNTSWMVEVNAK			177
Db	425	RVAPHDPLSL-KVKDI--NSTVIVTFMWLPG-----	-----NTKINLLQIETICKAN		469
OY	178	NRKD-----KNQTYNLT--GLQPTTEVIALRCVAKESKEFMSDSOQKMGMTREEA			226
Db	470	SKKEVRNATINGAESDYTHAVADKNPITATYFPRGSKTFPMKMSRMSDEKRLHITTEAT			529
OY	227	PC-GLEIMRLVLPKPAEADGRPRVRLIKKARQAPYLE--KTLGVINIWIYPESANTNLTEPM			282
Db	530	PSKGDPTWR---EMSSDCKNLI-YVWKP--LPINEANGKILSYVSCSLNEETQSVLEI			582
OY	283	NTNNOGLELHGGSEFWMSISYNSLGSP---VATLIRPAIQEKSFCIEVMQACVAD			339
Db	583	FDPOHRAIRIQSKNDYIISVAVARNASGSPSKRTIASMEIPN-----DITVEQAVVGLGN			636
OY	340	QLVVMQSSALDVNTWMIEMFEPDVSSEPTTSLMESVY--SQATNMWITQOQKLPFWCYNISV			398
Db	637	RIFLWRHDPMTWCDYAIKMCNSSSEBCLDMKRVPSNISTEYVIESQFPQGVATNYL			696
OY	399	YPLMCHDKVGEPSYIOAVYAKGVSEGPETKVENIGCVATVTYTWKEIPEKSRGGIICNNTI			458
Db	697	YGCTNOGYQLRSLIIGYVEELAPIVAPNFTVEDTSADSLIKWMDIIPHEELRGFLRGY-L			755
OY	459	FYQAEGGGFGSKT-----	-----VNSSILOGLGSLAKKSTSYIQVAMSTAG		501
Db	756	FYFOGGEADPTKRSLEPHHSDIKIKNTISQKTLR--IADLQKTSYHILAVRYTHGG			813
OY	502	GTNGRSINFKTLSEFVEIILITSLIGGLLILILLYAVAGL-----	-----KKPNKLT		550
Db	814	LGPEKSMVYVIREKNV-----	-----GLIALLIPVAVAVIYGVNISILCYRRKREMK		861
OY	551	HLCEFTVNPRESSIATYHGDQFKDLKLKESDOSVNTEDIRLKCPSPSKLVLD--KL			608
Db	862	ETFYEDIPDINPEKCKALQF-----QKSVCEGSNALKTLE--MNPC-TPNNVEVLESRSI			911
OY	609	VVNGNGVLOELFTDA--RTGOENNNGKRGKNGVT--CP-----FRPDC-----			.648
Db	912	VPKIEDT--ETISPAERPERGESEVDPPNNHVAVSYCPPIIEEITTPNPADEVGASQVYV			969

Qy	649	-----PLKSRTEE-----	-----LPVSEIPPRKSKYLSRMPDEGRPREAK	684
Db	970	IDVQSMTPQAKAAEEODVDVYVAGYKPKQMRLLIPSPAVEDTAEDEBGK-TAGYRRQAN	1028	
Oy	685	EQLFFSGSLVDP-----HICEGAPNPYLKNSVTAREFLVSEK	723	
Db	1029	---VNTNMLVSPDESPRSDSNNEVYSFSGP-----CSINSQFLIPRK	1068	
RESULT 8				
ID	1125_MOUSE	STANDARD:	PRF:	874 AA.
NC	P97378:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).			
GN	IL12RB2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
RN	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A. PubMed-8943050;			
RX	MEDLINE=97098510;			
RA	Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,			
RA	Gately M.K., Gubler U.;			
RT	"A functional interleukin 12 receptor complex is composed of two			
RT	beta-type cytokine receptor subunits."			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).			
CC	-1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A			
CC	LOW AFFINITY.			
CC	-1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH			
CC	AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND			
CC	IL12RB2.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-1- SIMILARITY: Contains 4 fibronectin type iii domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U64199; AAB36676.1; -			
DR	MGD: MGI:1270861; IL12RB2.			
DR	InterPro: IPR002896; CRIA.			
DR	InterPro: IPR003961; FN_III.			
DR	InterPro: IPR003529; Hemtopopn_L_F2.			
DR	Pfam: PF00041; fn3; 4.			
DR	SMART: SM00060; FN3; 4.			
DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.			
RW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.			
FT	SIGNAL	1	20	
FT	CHAIN	21	874	
FT	DOMAIN	21	639	
FT	TRANSMEM	640	656	
FT	DOMAIN	657	874	
FT	DOMAIN	137	230	
FT	DOMAIN	240	322	
FT	DOMAIN	436	523	
FT	DOMAIN	534	622	
FT	CARBOHYD	48	48	
FT	CARBOHYD	101	101	
FT	CARBOHYD	114	114	
FT	CARBOHYD	142	142	
FT	CARBOHYD	151	151	
FT	CARBOHYD	169	169	
FT	CARBOHYD	179	179	

Query Match	Best Local Similarity	9.9%: Score 385; DB 1; Length 874;	23.5%: Pred. No. 2,3e+21;
Matches 188;	Conservative 115;	Mismatches 316;	Indels 180; Gaps 38
QY 15	KPSLAALPAKEDNISCVYYRK-NITCWSPEKETSY-TQYTVKRTYAGEKHDCNTNS	72	
Db 130	EISGVAPPEPNQISCVOEGENGTVACSMNSGKVTYLTKNYTLQLS---GPNLLTC-QKQ	185	
QY 73	STSENRACSFPLPRIT-PP---NYTIEVAENGDOYIKSHMYTLEINAKTERPKI	127	
Db 186	CFSDNRQCNRLDGLINSPDLAESRFIVRYAINDLGSSSLPHTFFLDIPIPLPMD	245	
QY 128	FRVFPVLGIKRMIOLEWIKPELAPSSDLKTYLRFRVNSTSMMEVNFANKRDKNQTN	187	
Db 246	IRINFLANGSGRGITQM-EDEGQVYLNQRI---QPLNSTSMNMYN-ATNAKGR---YD	296	
QY 188	LTGLQPTTEVYIALCAVAKES-KFWSDMSQEKMGTETEEBAPCG-LELMVRLPAEADGR	245	
Db 297	LRLDRPFEYEFGQISSKHLHSGMSNMNSSELRTRPREEPYGLIDIWMKQDIOYD-RQ	355	
QY 246	PVRLIMTKARAGAPVLEKTLGNINWYPPESNTNLTETMNTTNQQLHELHGSEFWYMSISY	305	
Db 356	QISTFWKSLNPESEARGKILHYQVTL-QEYTKRTTLQMTNR-----HTSMTRVPI-	403	
QY 306	NSLGGSPATRIAPALOEKSFQOC---IEWMQACVA-----EDQLVYWKQ--	346	
Db 404	----RTGAWTASVSANSKSGASAPRHINIVDLGCGGLAPHOVASKSEMDNIIYTMQRP	459	
QY 347	---SSALDVNTWMIEM-----FPDYSEPTTLWSVESQATNMTIQQDKLFWPC	393	
Db 460	KKADSA-VREYIVEMRALOPGSIYKFPF-----HWLRIPPNMSALISENIKPYIC	509	
QY 394	YNISVYPLMLHKVGPYSIOAYAKGCVSEGEPTVENIGVATVITTKELPKSEKGTII	453	
Db 510	YEIRH-ALSESQGGCSSIRGDSKHKAPVSGCHTAITEKKERLFIWTHIPFPDQRCI	568	
QY 454	CNYTIFYOAEQKGC-----FSKTVNSSILOGLSLKRTSYIYQVMASTAG-GTN	504	
Db 569	LHYHTYKMERSTAQPELCEIOYRRSQNS---HPISLQRPVITYVLMNTATYTAGESQ	624	
QY 505	GTSINFTKLSVFEIILITSLDIGGILLIILVA-----YGLKKPNKTLHLCMP---	555	
Db 625	GNREDFCPOGAKNMKAFVYS-----ICIAITIVGTFISIRFROKAFLLSTLKPQWS	678	
QY 556	-TVNPPAASSIATYMHGDFKDKLNKESDSDVNTEDRIKLPESTPS--DKLVYDKLVNPF	612	
Db 679	RTIDPPAPS---TW-----VKKYPLEKIQDLP-DNLLMAMPTEEBERPLIINEHLYHM	729	
QY 613	GNVLOEIR-----PDEARIGQNNNIGGEKNGVYVCPF	644	
Db 730	IPVVRQPIYFRKGGCFQGYSTSKQDAMIANDQATGTLTAETROLVNL-----YKVLSS	783	
QY 645	R-PDQPLKSFEEELPVSP-EIIPRKSOYLRSRMPEGRPEAK-----	684	
Db 784	RDPQSKLANLSPILVTPVYVNLPSHNEGLLPSNIEDLSHDEADPTSPFDLEHONISLSIFA	843	
QY 685	----EQLLFSGQSLVPHL 699		
Db 844	SSSLRPLIFGGERLTLDRL 862		

RESULT 9

112S-HUMAN

ID 112S-HUMAN

STANDARD:

862 AA.

PRT:

862 AA.

AC Q99665; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).
 GN IL12RB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y., Gately M.K., Gubler U.;
 RA "A functional Interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.
 CC -1- SUBUNIT: DIMER/OLIGOMER: DISULFIDE-LINKED. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL; U64198; AAB3675.1; ...
 DR HSP; P40189; IBOU.
 DR Genew; HGNC:5972; IL12RB2.
 DR MIM; 601642; ...
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004907; P: interleukin receptor activity; TAS.
 DR GO; GO:0007166; P: cell surface receptor linked signal transdu. ; TAS.
 DR GO; GO:0008284; P: positive regulation of cell proliferation; TAS.
 DR InterPro; IPR002996; CRI1.
 DR InterPro; IPR003529; Hemtopoptn_L_F2.
 DR Pfam; PF00041; FN3; 3.
 DR SMART; SM00060; FN3; 4.
 KW PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 862
 FT DOMAIN 22 624
 FT TRANSMEM 625 641
 FT DOMAIN 642 862
 FT DOMAIN 224 306
 FT DOMAIN 421 508
 FT DOMAIN 519 607
 FT CARBOHYD 48 48
 FT CARBOHYD 129 129
 FT CARBOHYD 166 166
 FT CARBOHYD 195 195
 FT CARBOHYD 271 271
 FT CARBOHYD 347 347
 FT CARBOHYD 376 376
 FT CARBOHYD 480 480
 FT CARBOHYD 480 480
 FT VARIANT 185 480
 FT VARIANT 420 420
 FT VARIANT 426 426
 FT VARIANT 426 426

FT VARIANT 465 465 G -> D (IN dbSNP:2307153).
 FT /FTid=VAR_014808.
 SQ SEQUENCE 862 AA; 97134 MW; 67C0E0DD468BD58 CRC64;
 Query Match 9.8%; Score 383; DB 1; Length 862;
 Best Local Similarity 22.8%; Pred. NO. 3.2e-21;
 Matches 184; Conservative 116; Mismatches 322; Indels 184; Gaps 38;
 QY 22 PAKENISCYVYRK-NLTCTSPGKETS-YTOTVRYTAFAFGKHNCNTNSTSNNRA 79
 DB 124 PEQPNLSCIOKGEQVACTWGERGDTLHYETLQLS--GPK-NLTWQCKCK--I 176
 QY 80 SCSEF-----LPRTIPDNYTIEVEAENGCVIKSHMTYRLNIAKTEPKIFRYPV 134
 DB 177 YCOYLDGIDNLTPEPSNNTAKTAVNSIGSSSLPSTFLDVIAPLPWDRIKFK 236
 QY 135 GIKRMIOEIMKPELAPVSDLYTLFRFVNSTSMVEVNF-AKNRDKNQYNTLTGL 192
 DB 237 ASVSRCITLYWRDEGLV-----LNRRLYRPSNSRLMMVYTKAKGRHD-----L 285
 QY 193 PTEYVIALGCAVRESK-FWSDMSQEKMGTEEEAPCG-LEIMRYLKPAEADGRPVRL 250
 DB 286 PTEYFQISKLHYGSDMSSESLRAQTPPEEPGLDVMYMKRHID-SKQSLF 344
 QY 251 WKARGAPVLEKTLGYNINWYPPESNTNLTETMTNTNOQLIELHGESFVWSMI----- 303
 DB 345 WKNSVSEARKILHYQV-----TLQEL--TGKAMQNTGHSMTTVPRTGNWA 394
 QY 304 ----SYNSLGRSPVATLRIPAIQESFOCLEWQACVA-----EDQLYVKW 345
 DB 395 VAASAANSKGS-----LPT-----RINIMNCEAGLAPROVANSANSEGMNLTW 441
 QY 346 QSSALD---VNTWMIW---FPDYDSPTLTSMVSQATNMTIQDRLKRFVNYISVY 399
 DB 442 QPPKDSVAQOEYVERREHLPGGDTQ-VPLNMLRSPPYNVALISENISKYETEIRV 500
 QY 400 PMLHDKVEPYSIOAVAKEGVSEGPETKVENIGKVTITTKETIPKSERGIICNTIF 459
 DB 501 ALSGDO-GGCSILGNKHKAPLSGPHNATTEKSGILSWSNIPVOEOMGCLLHYRIY 559
 QY 460 YQAEKGK-----FSKYVNSSTLOYGLESLKRSYIYOVAASISAG-GTNGSTINF 510
 DB 560 WKERDSNSOPOLCIPRYVSONS---HPINSLQPRVTVYLMVMTALTAAGSSHGNREF 615
 QY 511 -----KTIQSVFEIILNISIGGLILILVLAAGKKPKNL-----THLCWPVNP 559
 DB 616 CLOGKAMMAFVAPISCAITIMVG-----ISTHYPQKVFVYLAALRPQKCSREIPD 668
 QY 560 PAESSIATWGDDEKDKLNLKESDVSNTEDRIKPCSTPSDKLVLDKLVVFGNVLOEI 619
 DB 669 PANSTCA-----KKYPIAEKTOQLPL-DRLLIDMPTPEDP--EPVVIS-EVLHY 714
 QY 620 FT-----DEARFGQENNLGCEKN-----G 638
 DB 715 TPVERHPPCSNMPREKGIQHOASEKDMHSASSPPPRALQAESQVLDVLYKVESRG 774
 QY 639 YVTPRPDDCLGKSFELPVSPETIPPKSQYLSRSRDEGRPAKQQLFSGOSLPVDH 698
 DB 775 SDPPENPACD---WVLPAGD--LPHDGYLPSNID--LPSHEAPLADSLTELEPOH 826
 QY 699 LCEGAPNPYLKNSVTAREFLVSEKL 724
 DB 827 ISLSVPS-----SSLHLPLTFSCGKL 848
 RESULT 10
 LEPR_RAT STANDARD; PRT; 1162 AA.
 AC Q62959; Q55772; Q53773; Q54805; P70493; P70494; P70495; P97589;
 AC Q62960; Q63007; Q63385; Q63386; Q9ERK14;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEPR OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
RC STRAIN-Zucker; TISSUE=Hypothalamus;
RX MEDLINE=96241565; PubMed=8673096;
RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
RA Hess J.F.;
RT "Leptin receptor missense mutation in the fatty Zucker rat.";
RL Nat. Genet. 13:18-19(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
RC STRAIN-Sprague-Dawley, and Zucker fatty; TISSUE=Brain;
RX MEDLINE=9629531; PubMed=8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Substitution at codon 269 (glutamine --> proline) of the leptin
RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
RT (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND E), AND VARIANT FA PRO-269.
RC STRAIN-Sprague-Dawley, and Zucker fatty;
RX MEDLINE=96332408; PubMed=8769097;
RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
RA Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary
RT DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)
RT rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM B).
RA Carlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
RA Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A), AND VARIANT FA PRO-269.
RC STRAIN-Sprague-Dawley, and Zucker fatty;
RX MEDLINE=96212906; PubMed=8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
RT Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC STRAIN-Sprague-Dawley; TISSUE=Spleen;
RA Park J.H., Ju S.K., Na S.Y., You K.H., Kim K.L.;
RT "Molecular cloning, sequencing, and recombinant expression of the long
RT form of the rat leptin receptor isolated from whole spleen RNA.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM F).
RC STRAIN-Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96368027; PubMed=8772180;
RA Wang M.-Y., Zhou Y.T., Newgard C.B., Unger R.H.;
RT "A novel leptin receptor isoform in rat.";
RL FEBS Lett. 392:87-90(1996).
RN [8]
RP SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
RT "Analysis of rat leptin receptor gene.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 557-802 AND 843-892 FROM N.A. (ISOFORMS C AND E).
RC STRAIN-Sprague-Dawley;
RX MEDLINE=97415825; PubMed=9268737;
RA Chien E.K., Hara M., Rouard M., Yano H., Philippe M., Polonsky K.S.,
RA Bell G.I.;
RT "Increase in serum leptin and uterine leptin receptor messenger RNA

RT levels during pregnancy in rats.";
RN Biochem. Biophys. Res. Commun. 237:476-480(1997).
RL [10]
RP SEQUENCE OF 694-878 FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Pancreas;
RA Ma Z.;
RT "Identification of a leptin receptor in islet.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE OF 821-894 FROM N.A. (ISOFORM A).
RC STRAIN-Mistar Munich; TISSUE=Kidney;
RA Totsune K., Takahashi K., Mackenzie H.S., Murakami O., Arihara Z.,
RA Sone M., Satoh F., Mouri T., Brenner B.M., Ito S.;
RT "Leptin receptor gene expression in rat kidney.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [12]
RP VARIANT FA PRO-269.
RX MEDLINE=96314329; PubMed=8690163;
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
RA Leibel R.L.;
RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
RT (Lepr).";
RL Diabetes 45:1141-1143(1996).
CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the
CC regulation of fat metabolism and in a hematopoietic pathway
CC required for normal lymphopoiesis. May play a role in
CC reproduction.
CC -I- FUNCTION: The short form (isoform A) may act to transport leptin
CC to the cerebrospinal fluid. The putative soluble receptor (isoform
CC E) could function as a transport protein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E
CC which could be secreted.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=6;
CC Name=B;
CC IsoId=O62959-1; Sequence=Displayed;
CC Name=A;
CC IsoId=O62959-2; Sequence=VSP_001705, VSP_001706;
CC Name=C;
CC IsoId=O62959-3; Sequence=VSP_001707, VSP_001708;
CC Name=D;
CC IsoId=O62959-6; Sequence=Not described;
CC Name=E;
CC IsoId=O62959-4; Sequence=VSP_001709, VSP_001710;
CC Name=F;
CC IsoId=O62959-5; Sequence=VSP_001711, VSP_001712;
CC -I- TISSUE SPECIFICITY: Isoform B is expressed in kidney, liver, lung,
CC ovary, spleen and uterus. Increased level in uterus during
CC gestation. Isoform F is expressed at high levels in liver and
CC spleen and less in brain, stomach, kidney, thymus, heart, lung and
CC hypothalamus.
CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-965 may be the
CC major site of phosphorylation. Phosphorylation on both sites is
CC required for full activity (by similarity).
CC -I- DISEASE: The fatty (FA) mutation produces profound obesity of
CC early onset caused by hyperphagia, defective nonshivering
CC thermogenesis, and preferential deposition of energy into adipose
CC tissue.
CC -I- SIMILARITY: Contains 3 fibronectin type III domains.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: U52966; AAC52587.1; -;
DR EMBL: D84550; BAA12697.1; -;
DR EMBL: D84551; BAA12698.1; -;

Query Match	Best Local Similarity	22.0%	Score 242.5	DB 1	Length 1162
Matches 170	Conservative 99	Mismatches 305	Indels 199	Gaps 42	
27 NISC-VYRRNLCTGSPGKETSYYQVYKRYAFGEKHNDCTNNS--					-TSEN-RASC 81
431 NISCETDYLTKMTCRMSPTQSLVSGTVOLRV-HRRSLYCPDNPSSIRPTSELK-NCV					487
82 -----SFLPRTTIPDNTTIEVLEANGCGVYKSHMTYRPLENIARTPEPKIRYRVPY					133
488 LQTDGEYECVQOP-IFLLSGYTMWIKRINHSLSGLSDSPPTCVLPDSVVRKLPPS-NVYAE					544
134 LGIKR-MIOIMWIPRELAPVSSDLKYTLRFRFVNSTSMWEVFAKRNKDKNQTYNULGLO					192
545 ITINNGGLKAVSEKRVFP--ENNDLFOFQIRGLNGKEIQMKTHEVVDANKSKSLVYSDL-					601
193 PTFEYVALKCAVNES-KFMSDWSOEKMGM-EEBAPC-GELMWYVLPKAEADGRRPVRL					249
602 -CAVYVYGVCRRLDGLGYGWSMSSPAYTLVADVVPVPMGPBFRIMDQITFKKRRNVTL					660
250 LMK-----KAGAPVLEKTLQYINWYVDESN-TNLT-----ETMNTNQDLHLHGG					295
661 LMKPLMKDLSCLSVARYVVKHRTAHNGTWSODVQGTNLTFLMASAHVTV-----LAI					715

Oy	296	ESFVWSMISYSLGKSPVATLRIPAIQEKSPQCEVWQACQAEQDLVVKMOSSLDVNT-	354
Db	716	NSIGASLNFENLFTSWPSS--KVAAYQ--SLSAYPLSSCC-----ILSTFLSPNDYSL	766
Oy	355	-WMEIEM--FPDVSDEPTTLISWESVSQATNMNTIQODKLKPFWCYNISVYPMILHKGEPYS	411
Db	767	YLVIEMKNLNDODG-----MKMLRIPSNVKNKYIHNDNIPLEKYQFSLYVFMGCVGPKI	822
Oy	412	IQAYAKGQVSESGE-----TKVENIGKVTVT-----ITWKEIPSEKGIIT	453
Db	823	INGTTKDDIKAKOQNDAGLYVLPILISSCVLLTGLTLISHQRMKMLPMDVDPNPKN----	878
Oy	454	CNTYTFQAEQEGKRFKSTVNSIIQYGLGELSLKRTSYIVQYMASTAGGNGTGINFKTL	513
Db	879	CSMA-----QGLNFKPKET-----	892
Oy	514	SFSYFEILL--ITSLIGGGLI-----LIITFYAYGLK--PKNLTHLCPTVNP	560
Db	893	----FEHLFTKHAESVIFGRLLEPERVSEISVDTMKKNKDEVPAAAMSILL-TTPDS	947
Oy	561	AESSIATWGHGDPFKDKLNLKESDSSVNTEDRIKPC-STPSDKLVLDKLVVFGNVLOEI	619
Db	948	TRGSIC-----ISDQNSANFSQAQSTQGTCEDECSQSPVKYA--TLVSN---VKTV	995
Oy	620	FTDAPRQGENNNGLEGKNGYTCFPRPDCPLGKSFEEELPSPLELPKKSQYLRSMEGT	679
Db	996	ETDEEQ-----CAIHSSVSQCLARKHSPRQSPSS--NSWELEDAQAFLLSDHPNVT	1046
Oy	680	RPEAKEOELFGSGSLVDPHLC-IGAPRPYLKNSVTAREFLVSEKLEPHTKGE	731
Db	1047	SP-----QLSFSGL---DELEELRG-----NFEENHGE	1072

RA Fischer A., Emile J.-F., Galliard J.-L., Meinel E., Casanova J.-L.,
 RT "Interleukin-12 receptor beta-1 deficiency in a patient with abdominal
 RL tuberculosis." ;
 CC J. Infect. Dis. 184:231-236(2001).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
 CC LOW AFFINITY.
 CC -1- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH
 CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
 CC IL12RB2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative products:
 CC Name-Long; Sequence-Displayed;
 CC Name-Short;
 CC IsoId=P42701-1; Sequence=VSP_001715;
 CC IsoId=P42701-2; Sequence=VSP_001715;
 CC -1- DISEASE: Defects in IL12RB1 are a cause of susceptibility to
 CC severe mycobacterial and Salmonella infections in otherwise
 CC healthy individuals.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
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 CC -----
 DR EMBL: U03187; AAA21340.1; ;
 DR EMBL: AJ297688; CAC10446.1; ;
 DR EMBL: AJ297689; CAC10446.1; JOINED.
 DR EMBL: AJ297690; CAC10446.1; JOINED.
 DR EMBL: AJ297691; CAC10446.1; JOINED.
 DR EMBL: AJ297692; CAC10446.1; JOINED.
 DR EMBL: AJ297693; CAC10446.1; JOINED.
 DR EMBL: AJ297694; CAC10446.1; JOINED.
 DR EMBL: AJ297695; CAC10446.1; JOINED.
 DR EMBL: AJ297696; CAC10446.1; JOINED.
 DR EMBL: AJ297697; CAC10446.1; JOINED.
 DR EMBL: AJ297698; CAC10446.1; JOINED.
 DR EMBL: AJ297699; CAC10446.1; JOINED.
 DR EMBL: AJ297700; CAC10446.1; JOINED.
 DR EMBL: AJ297701; CAC10446.1; JOINED.
 DR PIR: I37892; I37892.
 DR Gene: HGNC:5971; IL12RB1.
 DR MIM: 601604; ;
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0016517; F: interleukin-12 receptor activity; TAS.
 DR GO: GO:0006888; F: transmembrane receptor activity; TAS.
 DR GO: GO:0006960; F: antimicrobial humoral response (sensu Inver. . .); TAS.
 DR GO: GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.
 DR GO: GO:0008284; P: positive regulation of cell proliferation; NAS.
 DR InterPro: IPR003361; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO. REC. L_F2; 1.
 DR Receptor: Transmembrane; Glycoprotein; Signal; Alternative splicing;
 KV Repeat; Polymorphism.
 FT SIGNAL 1 23
 FT CHAIN 24 662
 FT DOMAIN 24 545
 FT TRANSMEM 546 570
 FT DOMAIN 571 662
 FT DOMAIN 43 133
 FT DOMAIN 143 236
 FT DOMAIN 237 337
 FT DOMAIN 338 444
 FT DOMAIN 445 540
 FT DISULFID 52 62
 BY SIMILARITY.

FT	CARBOHYD	121	121	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	329	329	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	346	346	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	456	456	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	659	662	KAKM -> DR (in isoform short).
FT	VARIANT	213	213	/FTid=VSP_001715.
FT	VARIANT	365	365	R -> W (confers susceptibility to mycobacterial and salmonella infections).
FT	VARIANT	378	378	/FTid=VAR_015577.
FT	VARIANT	378	378	M -> T (in dbSNP:373947).
FT	VARIANT	378	378	/FTid=VAR_011986.
FT	VARIANT	378	378	G -> R (in dbSNP:401502).
FT	VARIANT	378	378	/FTid=VAR_011987.
SO	SEQUENCE	662 AA; 73108 MM; 541ADA60F62DAA1EF CRC64;		

Query Match 5.9%; Score 231.5; DB 1; Length 662;
 Best Local Similarity 21.7%; Pred. No. 8.4e-10;
 Matches 149; Conservative 96; Mismatches 253; Indels 189; Gaps 34;

QY	8	WMLPSLCKFSLAALPAK-----PENISCVYYRRKULTCWSP 44
DB	7	WVVPILFLFLSLRQGAACRTSECCFODPPRPDADSGSAGPRDLRCYRISSDRXCSWOY 66
QY	45	GKETSTYQYTVKRTYAFGEKHNDCTTNSSTSENASCSEFLPRITIPDNTYIE--VEAEN 102
DB	67	ECPTAGVSHRLRCLSLSG-----RCGYFAAGSATRLQ---FSDAGSVLTATVLMWESNA 119
QY	103	GQGVKSHMTWYMLENAKTERP-KIFRYKPVGLTRMIOEIKPELAPVSSDLKYTLR 161
DB	120	RNOTKSPREYTDLYNSVKYEPGLDGIKSKLGLQRLM--EWETPD-NQVGAEOVF--R 173
QY	162	FRTVNSTSW-----MEVFAKNKKKKNQYVNLGLDPFTGYVALNC 203
DB	174	HRT-PSSPMKLGDCGQDDDTESCLPRLMNAQ-----EFQLRHQ 214
QY	204	AYKESKFNQDMSQ-----EKMG-----MTEEPAGLEIMRLKPA 239
DB	215	LGSQGSWSKSSPVCVPPENPPQPVQRFSEVQLGDDGRRLTLKQPTQLEL-----PE 269
QY	240	EADGRPRVRLMKKAGAVLEKTLGYNLWYRPESNTNLTEMTNTNOGLEHLG----- 294
DB	270	GGQGL-----AGTEVT--YRLQLHMLSCPCAKAKTRT-----LHLGKMPYL 309
QY	295	-GESEFWMSIYNSLKSFPVATLRIPALOEKSFQCEVQACVACEDQVVKWQSSALDVN 353
DB	310	SCAAVYVAIVISSNOGPGNLQNTWHLIPADHTHPVALNT---SVGTNGTMTYPARAOSH- 365
QY	354	TMMIEMFP-----DVSEEP---TTLSEWSYQATMTNTIQQDKLPKWCYNI 396
DB	366	TYCISWOPVGGDGLATGSLTAPODPDAGMATYSSMSRSGA-----MGEK-----CYII 416
QY	397	SVYPMILHKVGEPPYS--IQAY-----AKEGVSPSGEPKEKVENICVKTVTITWKETIPSE 448
DB	417	TIFSAHPEKLTLMSTVSLTYHEGNSASAGPRH--HVSQKNSHLSDSVDMAPSLST 473
QY	449	RKGIICNTTYFYQAEGRGFSK-TYVSSILQGLESLKRTSYIQVMASTN-AGTNGT 506
DB	474	CPGVLEKVVVACRDEDSQVSEHNPQPTETVTLTSLGALGAVYATVQVADTAMLRGWSQ 533
QY	507	SINRTLSFSVEIITLITSLIGGLLILITVAV-GLKRNKLTNLCMPVNPFAESSI 565
DB	534	QPRF-SIEVQVSDWLIFFASLGSFSLVGLVGLGLNRAAR--HLC-PLPPTPCASSA 589
QY	566	ATWHD-----DPKDKLNKES 582
DB	590	IEFPGKETQWIMNPVDQEBASLQEA 616

RESULT 12
 LEPR_MOUSE
 ID LEPR_MOUSE STANDARD: PRT; 1162 AA.

AC P48356: 035686; 054986; 061215; 064309; 090M3; 090W5;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219).
GN LEP-R OR OB-R OR DB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI-TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Meng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R";
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Wolf E.A., Weng X.,
RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT "Identification of a mutation in the leptin receptor gene in db/db
RT mice";
RL Cell 84:491-495(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=96231997; PubMed=8628397;
RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
RA Lee J.I., Friedman J.M.;
RT "Abnormal splicing of the leptin receptor in diabetic mice";
RL Nature 379:632-635(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC STRAIN=BA1B/C; TISSUE=Liver;
RX MEDLINE=96206286; PubMed=8616721;
RA Clouff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
RA Mikhail B.I., Plavika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction";
RL Nat. Med. 2:585-589(1996).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC STRAIN=NZO; TISSUE=Hypothalamus;
RX MEDLINE=97462708; PubMed=9322835;
RA Igel M., Becker W., Herberg L., Joost H.G.;
RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
RT in the New Zealand obese mouse";
RL Endocrinology 138:4234-4239(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC STRAIN=FVB/N; TISSUE=Spleen;
RX MEDLINE=96270520; PubMed=8692797;
RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Helm M.H.,
RA Skoda R.C.;
RT "Defective STAT signaling by the leptin receptor in diabetic mice";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND E).
RC STRAIN=129/J;
RX MEDLINE=98008913; PubMed=9344648;
RA Chua S.C., Koutas T.K., Han L., Liu S.M., Kay J., Young S.J.,
RA Chung W.K., Leibel R.L.;
RT "Fine structure of the murine leptin receptor gene: splice site
RT suppression is required to form two alternatively spliced
RT transcripts";

RL Genomics 45:264-270(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT ASN-600.
RC STRAIN=KK Obese; TISSUE=Hypothalamus;
RX MEDLINE=99061814; PubMed=9845674;
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
RA Joost H.G.;
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
RT hyperinsulinemic KK mouse strain";
RL J. Endocrinol. 21:337-345(1998).
RN [9]
RP SEQUENCE OF 890-1162 FROM N.A. (ISOFORM B).
RC STRAIN=129;
RA Banks A.S., Myers M.G. Jr.;
RT "Murine leptin receptor genomic exon 1b and surrounding sequence";
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
RN [10]
RP PHOSPHORYLATION OF TYR-985 AND TYR-1138, AND MUTAGENESIS OF TYR-985;
RP TYR-1077 AND TYR-1138.
RX MEDLINE=20261588; PubMed=10799542;
RA Banks A.S., Davis S.M., Bates S.H., Myers M.G. Jr.;
RT "Activation of downstream signals by the long form of the leptin
RT receptor";
RL J. Biol. Chem. 275:14563-14572(2000).
CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the
CC regulation of fat metabolism and in a hemopoietic pathway
CC required for normal lymphopoiesis. May play a role in
CC reproduction.
CC -I- FUNCTION: The short form (isoform A) may act to transport leptin
CC to the cerebrospinal fluid. The putative soluble receptor (isoform
CC E) could function as a transport protein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E
CC which could be secreted.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=5;
CC Name=B;
CC IsoId=P48356-1; Sequence=Displayed;
CC Name=A;
CC IsoId=P48356-2; Sequence=VSP_001697, VSP_001698;
CC Name=C;
CC IsoId=P48356-3; Sequence=VSP_001699, VSP_001700;
CC Name=D;
CC IsoId=P48356-4; Sequence=VSP_001701, VSP_001702;
CC Name=E;
CC IsoId=P48356-5; Sequence=VSP_001703, VSP_001704;
CC -I- TISSUE SPECIFICITY: Isoform A: highest level of expression in lung
CC and kidney, also present in kidney, heart, brain, spleen, liver,
CC muscle, choroid plexus and hypothalamus. Isoform B: highest level
CC of expression in hypothalamus and lower level in brain, testes and
CC adipose tissue. Isoform E: expressed in adipose tissue,
CC hypothalamus, heart, and testes.
CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the
CC major site of phosphorylation. Phosphorylation on both sites is
CC required for full activity.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: Contains 3 fibronectin type III domains.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U42467; AAA93014.1; -;
DR EMBL: U46135; AAC52408.1; -;
DR EMBL: U49106; AAC52420.1; -;
DR EMBL: U49107; AAC52421.1; -;
DR EMBL: U49108; AAC52422.1; -;
DR EMBL: U49109; AAC52423.1; -;
DR EMBL: U49110; AAC52424.1; -;

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
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 CC -----
 DR EMBL: U23922; AA87457.1; -
 DR PIR: I49295; I49295.
 DR MGD: MGI:104579; I112r1.
 DR InterPro: IPR003963; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SMO0060; FN3; 1.
 DR ProSITE: PS01353; HEMATOPO. RECL_F2; FALSE NEG.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 738 INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.
 FT DOMAIN 20 565 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 566 591 POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 592 738 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 44 142 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 152 258 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 259 359 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 360 465 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 467 553 BY SIMILARITY.
 FT DISULFID 53 63 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 50 50 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 738 AA; 81661 MW; 05D7AC306F1059CE CRC64;

Query Match 5.8%; Score 226; DB 1; Length 738;
 Best Local Similarity 20.1%; Pred. No. 2.6e-09;
 Matches 163; Conservative 113; Mismatches 309; Indels 224; Gaps 37;

OY 22 PAKENINSCVYYIKNLCTW---SPGKESITYOYKRYAFGEKHDNC---TTNSSTS 75
 DB 45 PLGRNINSCVYKVSSTDECSWQYDGPEDNVSHVLMC---CVPRPHHTGTG 91
 OY 76 ENRASCSPF-----LPRITPDNTTIEVANGGVKSHMTYRLLENIAETE 123
 DB 92 QER--CRFFSSGPRPTVOFMEODGIPVLSKYNFWEESRLGRNYSOKISOYLNTWTTT 149
 OY 124 PKRIEYKPVLGIRKMTQIEMIKPELAVSSDLKYTLTFRFVNSTSWMEVFAKRNKDKN 183
 DB 150 PP-LGHK-KVSQSHQGLRMDW-----NVSEAGAEVQFRRMPTTN 188
 OY 184 QTYNLGTGQPTT-EVYIALRC-AVKESEF-----WSDWS 215
 DB 189 WTLGDCGQVNVSGGVADLDIGCSWSESCIPSENAOIEIQRRLRLSSGAPGFWSDWS 248
 OY 216 QEKGMTEEPAPCGLELRLVLPAPADGR-----PVALLMKKARGAP-----V 259
 DB 249 M-PCVPEVLP-QAKIFELVEPLNCGRRRLTMOGOSPOLAVEGCGRGRAOVKKLIV 306
 OY 260 LEKTLGVNIWYPPSNNTLFTMTNTNOQLHLHGSEFWWSMISYNSIGKSPVATLRIP 319

DB 307 LVRL-----SCRQAOQTSKTVPLGKLNLSGATYDLNLVLAKEFRGSTIOKMLP 357
 OY 320 AIOEKSPCIEVMACVAEDLVKMOSSALDVNTMIEWP-----D 362
 DB 358 AOELTETRLNV---SVGGNMTSMQMAQA-PGTYTLCLEWQPMFOHRNHTCLIVPEE 413
 OY 363 VDSEPTLMSVSVQATWITQODKLPFCMYNTISVY-----PMLDKGEPYSIQAY 415
 DB 414 DPAKMYHSMWSKP-----TLEQEE-----CYRITVFASKRPKPMMLATVLSYRGN 463
 OY 416 A-KGVDSGEPETVEVNIKVTVITTKKEIPKSERKGIICVYITFYQAEGKGFSK-TVN 473
 DB 464 ASRAGTPR---HVSVRNQTGDSVEMTAQSLSCTCPGVLTQYVVRCEADEGAMSEMLVP 520
 OY 474 SSIIQGLSELSKRTSYIVQYMASTAGTGTSTINFTLSFSV--PEIILITSLIGGL 531
 DB 521 PTKQVYTLDLGRLSRMKRVQVRAOTAR--LPGAMSHPORFSEVOISRLSTIFSLGSA 578
 OY 532 LILITFYAY-GLKKPNKLTLCWPTVNPASSIATWHGDDPKDKLNKESDSVNTED 590
 DB 579 SYLVGSLGTYGLNR--AAHLC-PPLPTPCGSTAVEPFGSGO-----KAMQMCNPD 629
 OY 591 RILPCSTPSDKLVYIDKLNVNFGVLOEIFTDEARTGOENMLGGEKNGYVTCPPRPDCL 650
 DB 630 --PEVLVPRDALVE-----MPGR----- 648
 OY 651 GKSEELPVSEIPEPKSQYRSRMPSECTREAKEQLFSQSLVPHLCEGAPN--- 706
 DB 649 GDGTESPOAEBECA-----LDTRPLETOROROVQALSEARL---GLAREDCPRGDLA 699
 OY 707 ---PYKNSVTAREFLVSEKLPETHKE 731
 DB 700 HTVLPILIGVYTGAGSVIDDLMRHKTRAE 728

RESULT 14
 CALC_MOUSE STANDARD: PRT: 3119 AA.
 ID 060847; P70322;
 AC 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DR 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(XII) chain precursor.
 GN COL12A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-1 AND XIIA-2).
 RC STRAIN=Swiss Webster, and C57BL/6J; TISSUE=Skin;
 RA MEDLINE=96170761; PubMed=8601036;
 RX Boehme K., Li Y., Oh P.S., Olsen B.R.;
 RA Olsen B.R., Nishimura I.;
 RT "Structural variation of type XII collagen at its carboxyl-terminal
 RT collagen XII and their tissue-specific expression during embryonic
 RT development.";
 RL Dev. Dyn. 204:432-445(1995).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-2 AND XIIA-2).
 RC STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
 RA MEDLINE=99348349; PubMed=10419532;
 RX Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W.,
 RA Olsen B.R., Nishimura I.;
 RT "Structural variation of type XII collagen at its carboxyl-terminal
 RT NCI domain generated by tissue-specific alternative splicing.";
 RL J. Biol. Chem. 274:22053-22059(1999)
 CC -1- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
 CC CONTAINING FIBRILS, THE COL1 DOMAIN COULD BE ASSOCIATED WITH THE
 CC SURFACE OF THE FIBRILS, AND THE COL2 AND NC3 DOMAINS MAY BE
 CC LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).
 CC -1- SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 KDA OF

QY 125 PKIFRKPVLGIRKMIQIEMIKPELAPVSSD-----LKYLRFRTVNST 168
 DB 713 ---FSV-PIEGEETIAEYKGV-PRNLKYTDDETDSFKLWSQAPGRVLRIRIRYPVSGG 767
 QY 169 SMVEYNFAKNRKNQYTNLTGLOPTEYVIALRCVAKESKFWSDWSEKMGMEDEAPC 228
 DB 768 ESKEVSFPANORR-----TLENLPDPDTKEYEISV-----IAEYPSGSGPLGNMATEEVR 818
 QY 229 GLELMRVLPKPAEADRRRVRLLMKKARGAPVLEKTLGNINMYPPSNNTNLETM---NTT 285
 DB 819 GNP--RDLRVSDAT-TSTLKLWSRAPG-----KVKQYLVTYTPAGGETQGVTVRGDTT 870
 QY 286 NOOLELHGSEFWWSMISYNSIGKSPATLRIPAIQKESFOCIEMVACVAD-----QL 341
 DB 871 TTMLRKLEGTQYDLSVNLALYASGGEALSGSGSLERGSP-----QNLVTKDITDTSI 925
 QY 342 VVKMOSSALDVNTMNIEM---PPVDSEPTLTSWESVSQATNMTIQDKLKEPWCYNISV 398
 DB 926 GAYWTSAPGMWAGYRVSWKSLYDDIEAGETTLNGDAITMI-----ENLQPEYKIKISV 979
 QY 399 YPMLHDKYGEPTSIQAVAKEGVPSGPEETKVENICVNTITMKELPKSEKGIICNTI 458
 DB 960 FATVSSGGEPT-VYGDATTELISQSKILRVDEEHEHTRVTKAP-----GKVVNRYV 1032
 QY 459 FYQAEAG-----KGFSTVNSIIOYGLSLKRTSYIVQVASTSAGTNGTSINFTL 513
 DB 1033 VYRPGGGRQWAKVPTVTSTV-----LKRLQPTTIDTIVLPM-----YKT- 1075
 QY 514 SFSVEIILLTSLGGCLLILTVANGKKPKNLT-----HLCWPTVPNPAESS 564
 DB 1076 -----GEGKLRQSGTJASFRKSPRLKTSDPMTSSFRVYWEPAPEVKGY 1121
 QY 565 IATWH--GDDEFK-DKLNKESDPSVNTEDRIKPCSTPSDKLVIKLVNFEVNOLEIFT 621
 DB 1122 KTFHPHTDDRLGELVLPDNTV-----VLEEL-- 1151
 QY 622 DEARTGOENNLGKENGNYVTCFPRDPCPLGKSFEEPLPSPEIPPKRSOYLRSMEGTERP 681
 DB 1152 -RAGTTRYVNVFGMFDGSGSLPL-----VCGEMTLTSDTTPV-----FLSSGMCLTRFA 1200
 QY 682 EAKEQLFSG 691
 DB 1201 EADIVLAVDG 1210

RESULT 15
 LEPR_HUMAN
 ID LEPR_HUMAN STANDARD: PRT: 1165 AA.
 AC P48357: Q13592: Q13594: Q92919: Q92920: Q92921:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (HUB219).
 GN LEP-R OR OB-R OR DB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS B AND E).
 RC TISSUE=Brain;
 RX MEDLINE=96128129; PubMed=8548812;
 RA Tartaglia L.A., Dembski M., Wang X., Deng N., Culpepper J.,
 RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
 RA Muir G., Sankar S., Moriarty A., Moore K.J., Smutko J.S.,
 RA Mays G.G., Woolf E.A., Montore C.A., Tepper R.I.;
 RT "Identification and expression cloning of a leptin receptor, OB-R.";
 RL Cell 83:1263-1274(1995).
 RN (12)
 RP SEQUENCE FROM N.A. (ISOFORMS A, B AND C).
 RC TISSUE=retal liver;
 RX MEDLINE=96398968; PubMed=8805376;
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,

RA Matthews W.;
 RT "A role for leptin and its cognate receptor in hematopoiesis.";
 RL Curr. Biol. 6:1170-1180(1996).
 RN (3)
 RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS ARG-109 AND ARG-223.
 RX MEDLINE=97301763; PubMed=9158141;
 RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;
 RT "Structure and sequence variation at the human leptin receptor gene in
 lean and obese Pima Indians.";
 RL Hum. Mol. Genet. 6:675-679(1997).
 RN (14)
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=97215244; PubMed=9061609;
 RA Luch S.-M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;
 RT "Cloning and characterization of a human leptin receptor using a
 biologically active leptin immunoadhesin.";
 RL J. Mol. Endocrinol. 18:77-85(1997).
 RN (15)
 RP SEQUENCE FROM N.A. (ISOFORMS A, C AND D).
 RC TISSUE=Retal liver;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shaler A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
 RA Platika D., Snodgrass H.R.;
 RT "Novel B219/OB receptor isoforms: possible role of leptin in
 hematopoiesis and reproduction.";
 RL Nat. Med. 2:585-589(1996).
 RN (16)
 RP ALTERNATIVE SPLICING DUE TO AN ENDOGENOUS RETROVIRUS.
 RX MEDLINE=99128223; PubMed=9929394;
 RA Kapitonov V.V., Jurka J.;
 RT "The long terminal repeat of an endogenous retrovirus induces
 alternative splicing and encodes an additional carboxy-terminal
 sequence in the human leptin receptor.";
 RL J. Mol. Evol. 48:248-251(1999).
 RN (17)
 RP CARBOHYDRATE-LINKAGE SITES, DISULFIDE BONDS, AND PARTIAL SEQUENCE.
 RX MEDLINE=99003211; PubMed=9786864;
 RA Hanlu M., Arakawa T., Bures E.J., Young Y., Hui J.O., Rohde M.F.,
 RA Welcher A.A., Horan T.;
 RT "Human leptin receptor. Determination of disulfide structure and
 N-glycosylation sites of the extracellular domain.";
 RL J. Biol. Chem. 273:28691-28699(1998).
 RN (18)
 RP VARIANT ARG-223.
 RX MEDLINE=96270489; PubMed=8666155;
 RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;
 RT "The hypothalamic leptin receptor in humans: identification of
 incidental sequence polymorphisms and absence of the db/db mouse and
 fa/fa rat mutations.";
 RL Diabetes 45:992-994(1996).
 RN (19)
 RP VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.
 RX MEDLINE=97289527; PubMed=9144432;
 RA Echalald S.M., Soerensen T.D., Soerensen T.I., Tybjærg-Hansen A.,
 RA Andersen T., Chung W.K., Leibel R.L., Pedersen O.;
 RT "Amino acid variants in the human leptin receptor: lack of association
 to juvenile onset obesity.";
 RL Biochem. Biophys. Res. Commun. 233:248-252(1997).
 RN (110)
 RP VARIANTS ARG-109; ARG-223 AND ASN-656.
 RX MEDLINE=97431549; PubMed=9287054;
 RA Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,
 RA Sothman M., Udall J.N., Kahle B., Leibel R.L.;
 RT "Exonic and intronic sequence variation in the human leptin receptor
 gene (LEPR).";
 RL Diabetes 46:1509-1511(1997).
 RN (111)
 RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
 RX MEDLINE=99075638; PubMed=9860295;
 RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,
 RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
 RT "Transmission disequilibrium and sequence variants at the leptin

RT receptor gene in extremely obese German children and adolescents.";
 RL Hum. Genet. 103:540-546(1998).
 RN [12]
 RP VARIANTS ARG-109; ARG-223 AND ASN-656.
 RX MEDLINE=97318795; PubMed=9175732;
 RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,
 RA Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
 RT "Leptin receptor gene variation and obesity: lack of association in a
 RT white British male population.";
 RL Hum. Mol. Genet. 6:869-876(1997).
 CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the
 CC regulation of fat metabolism and in a hematopoietic pathway
 CC regulated for normal lymphopoiesis. May play a role in
 CC reproduction.
 CC -I- FUNCTION: The short form (isoform A) may act to transport leptin
 CC to the cerebrospinal fluid (By similarity).
 CC -I- SUPRACELLULAR LOCATION: Type I membrane protein. Except for form E
 CC which could be soluble.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=5;
 CC Name=A; Synonyms=13.2, OBRD;
 CC IsoId=P48357-1; Sequence=Displayed;
 CC Name=B; Synonyms=6.4, HUB219.3;
 CC IsoId=P48357-2; Sequence=VSP_001689, VSP_001690;
 CC Name=C; Synonyms=12.1, OBRa;
 CC IsoId=P48357-3; Sequence=VSP_001691, VSP_001692;
 CC Name=D; Synonyms=HUB219.2;
 CC IsoId=P48357-4; Sequence=VSP_001693, VSP_001694;
 CC Name=E;
 CC IsoId=P48357-5; Sequence=VSP_001688;
 CC -I- TISSUE SPECIFICITY: Isoform A expressed in fetal liver and in
 CC hematopoietic tissues and choroid plexus. In adults highest
 CC expression in heart, liver, small intestine, prostate and ovary.
 CC Low level in lung and kidney. Isoform B is highly expressed in
 CC hypothalamus.
 CC -I- DOMAIN: The cytoplasmic domain may be essential for intracellular
 CC signal transduction by activation of JAK tyrosine kinase and
 CC STATs.
 CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-986 may be the
 CC major site of phosphorylation. Phosphorylation on both sites is
 CC required for full activity (By similarity).
 CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -I- SIMILARITY: Contains 3 fibronectin type III domains.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 DR EMBL: U43168; AAA93015.1; -;
 DR EMBL: U66495; AAB07495.1; -;
 DR EMBL: U66496; AAB07496.1; -;
 DR EMBL: U66497; AAB07497.1; -;
 DR EMBL: U59263; AAB09673.1; -;
 DR EMBL: U59248; AAB09673.1; JOINED.
 DR EMBL: U59249; AAB09673.1; JOINED.
 DR EMBL: U59250; AAB09673.1; JOINED.
 DR EMBL: U59252; AAB09673.1; JOINED.
 DR EMBL: U59253; AAB09673.1; JOINED.
 DR EMBL: U59254; AAB09673.1; JOINED.
 DR EMBL: U59255; AAB09673.1; JOINED.
 DR EMBL: U59256; AAB09673.1; JOINED.
 DR EMBL: U59257; AAB09673.1; JOINED.
 DR EMBL: U59258; AAB09673.1; JOINED.
 DR EMBL: U59259; AAB09673.1; JOINED.
 DR EMBL: U59260; AAB09673.1; JOINED.
 DR EMBL: U59261; AAB09673.1; JOINED.
 DR EMBL: U59262; AAB09673.1; JOINED.
 DR EMBL: U50748; AAC23650.1; -;

DR EMBL: U52912; AAC50509.1; -;
 DR EMBL: U52913; AAC50510.1; -;
 DR EMBL: U52914; AAC50511.1; -;
 DR HSSP: P16471; 1BP3.
 DR Gene: HGNC:6554; LEPR.
 DR MIM: 601007; -;
 DR GO: GO:0004888; F:transmembrane receptor activity; TAS.
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu...; TAS.
 DR GO: GO:0007275; P:development; TAS.
 DR GO: GO:0006112; P:energy reserve metabolism; TAS.
 DR InterPro: IPR002966; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR InterPro: IPR007110; Ig-like.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 4.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 DR PROSITE: PS00835; IG-LIKE; 1.
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; Alternative splicing; Phosphorylation;
 KW Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 1165 LEPTIN RECEPTOR
 FT DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 840 862 POTENTIAL.
 FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 325 429 IG-LIKE.
 Query Match 5.7%; Score 221; DB 1; Length 1165;
 Best Local Similarity 19.2%; Pred. No. 1.2e-08;
 Matches 142; Conservative 121; Mismatches 296; Indels 180; Gaps 34;
 27 NISC-VYYRKNLCTWSPGKSTSTQYTKTFAFGKHNDCTNSS----- 73
 433 NISCETDGLTKMTKRWSTTQSLAESTLQIRYRSSLY--CSDIPSTHPISEPKCYL 490
 74 TSENKSCFELPRITIPDNTIEVEAENGDSVIRSHMTYMRLENIAKTEPKIRVAPV 133
 491 OSDGYECIF--QPIFLSGYTMWRIRHNSLGSLSDPCTVLPDSVAVLPSSVKAELT 548
 134 LGIKMTDIEWKPEPLAVSSDLKTLRP-RVNSTSW--MEVNAKAKRKDKNOTYNLTG 190
 549 INI-GLIKRISWEKPEP--ENNLOPQIRYSGKEVQMKMEVYDAKSKSVLPVPCA 605
 191 LQPFVEYIALRCAVAKES-KFMSDSQKMGKTEE-EAPC-GLDLRWLKRPEADGRPV 247
 606 V-----YAVQYRCKRLDGLGYSMNSNPATYYVMDIKPKRPFWRRIINDTKKKNV 660
 248 RLWKKARGAPVLEKTLGYNIMYYPESNTNLTETMNTNQOLEHLGSEFW-----VS 301
 661 TLMKRLPKKNDSLCSGVRVIVNHNSCN-----GTWSEDEVGNHTKFTFLWTEQAHVY 713
 302 MISTVSLGK-----PVATLRIPAIQKESQCLIEWQACVADQLVYKKQSSALD 351
 714 VLAINSIGASVANFNLTSPMSKVN-----VQSLSAVPLNNSCV-----IYSWLSPSD 764
 352 VNT--WMIETPDDVSEPTTSMESVSQATMWTIQDGLKPKWCNISVYPLJHKGVEP 409
 765 YKMKFTIEW--KNINDEGELKWLRISSVKKYIYHDFIPEKTYQFSLYTFPMEGVGRP 822
 410 YSIQAYAKEGVSESEPE-----TVENIGVATVT-----ITMKRPTKSEKRG 451
 823 KIINSFTQDDIEKHQSDAGLYVIYVLISSILLGLTLLISHQKAKLFWEDVPRPKN-- 880
 452 IICNTTIFYQADGKGFSK-----TVNSIIQYGL--ESLKRKTSY----- 490
 881 --CSWA-----OGINFOKPETFEHLFIKHTASVYCGPLLEPETISDIDSVDTSKMKND 932
 491 -----IYQVWASTS-ACGTNGTSTINEKTLSESVFEIILLISLIGGLILLIILVANG 543
 933 EMPTTVSLSTLDLEKGSVCISDQFNSVNSEAEGETVEYEAESQROPFVKYATLLSN 992

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OY 544 KKP-----NKLTHLCPVTPNPAESSI--ATWGDDEKDKLNLKESDSDSYNTEDR 591
Db 993 SKPSETGEQGLINSSVTKCFSSKNSPLKDSFNSNSW---ETBAQAFILSDQHFN----- 1045
OY 592 ILKPCSTPSDKLVIDKLVNFGNVLOE-----IFTDEARTGOE 629
Db 1046 IISPHLTFSEGL--DELLKLEGNFPEENNDRKSIYILGVTSIKKRESGVLLTDKSR----- 1099
OY 630 NNLGGEKNGYVTCPPRPDC 648
Db 1100 -----VSCPPRPAC 1108

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Search completed: August 4, 2003, 11:23:16
 Job time : 31 secs

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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:20:22 ; Search time 111 seconds
(without alignments)
1701.752 Million cell updates/sec

Title: US-09-892-949-2
Perfect score: 3908
Sequence: 1 MMWTWALMLPCLCKFSLAA.....VFARFLVSEKLPHETKGEV 732

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3908	100.0	732	4	08N117
2	2635.5	67.4	509	4	08WY10
3	2132.5	54.6	716	11	08K5B1
4	2128.5	54.5	716	11	08R501
5	707.5	18.1	918	13	09W609
6	664.5	17.0	235	11	08BSU3
7	620.5	15.9	881	13	057519
8	606	15.5	710	13	057520
9	430.5	11.0	848	6	08W24
10	425.5	10.9	861	6	08M51
11	412.5	10.6	861	6	09BEG2
12	395.5	10.1	1093	11	070535
13	375	9.6	979	4	099650
14	361	9.2	1083	13	080F07
15	343	8.8	970	11	088821
16	342.5	8.8	971	11	070458

17	247	6.3	623	11	070394	070394 mus musculu
18	233.5	6.0	1147	13	09DDK1	09ddk1 melaeagris g
19	233	6.0	422	4	09UHH5	09uhb5 homo sapien
20	233	6.0	422	4	075462	075462 homo sapien
21	232	5.9	1148	13	091BA7	091ba7 homo sapien
22	231	5.9	425	11	09JW58	09jw58 mus musculu
23	216	5.5	2222	5	097394	097394 drosophila
24	213	5.5	1146	13	091RW6	091rw6 gallus gall
25	207	5.3	636	4	060624	060624 homo sapien
26	207	5.3	1212	4	095TC0	095tc0 drosophila
27	207	5.3	2016	5	08MKY7	08mk7 drosophila
28	207	5.3	2016	5	08MKM6	08mk6 drosophila
29	207	5.3	2016	5	09NBA1	09nba1 drosophila
30	207	5.3	2019	5	08MKM8	08mk8 drosophila
31	204	5.2	2221	5	09UIM1	09uim1 drosophila
32	197	5.0	152	6	09N18	09n18 meacaca mula
33	196.5	5.0	608	11	099J21	099j21 mus musculu
34	194.5	5.0	1723	11	08CHB2	08chb2 mus musculu
35	194	5.0	292	11	08C7G1	08c7g1 mus musculu
36	193.5	5.0	629	4	08NFC9	08nfc9 homo sapien
37	193.5	5.0	1842	4	081ZY3	081zy3 homo sapien
38	193.5	5.0	2053	4	08WU7	08wu7 homo sapien
39	193.5	5.0	2053	4	081ZY4	081zy4 homo sapien
40	193.5	5.0	2113	4	08TD84	08td84 homo sapien
41	193	4.9	26926	4	08WZB3	08wzb3 homo sapien
42	193	4.9	34350	4	08WZ42	08wz42 homo sapien
43	192.5	4.9	1232	13	090284	090284 carassius a
44	190.5	4.9	1898	11	09ED17	09ed17 mus musculu
45	190	4.9	4280	5	09UB29	09ub29 caenorhabdi

ALIGNMENTS

RESULT 1
08N117
ID 08N117 PRELIMINARY; PRT; 732 AA.

AC 08N117;
DT 01-OCT-2002 (TREMBLrel. 22. Created)
DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Gp130-like monocytic receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21988187; PubMed=11877449;
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals Proliferation, and Activates STAT-3 and STAT-5.";
RL J. Biol. Chem. 277:16831-16836(2002).
DR EMBL: AF466620; AAM27958.1;
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 3.
KW Receptor.
SO SEQUENCE 732 AA; 82953 MW; 30F84BD3DD99A20E CRC64;

Query Match 100.0%; Score 3908; DB 4; Length 732;
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QY 61 FGEKHDNCTTSSSENASCSPFLPRITTDNTTIEVEANGGVKSHMTYVRLNIA 120
DB 61 FGEKHDNCTTSSSENASCSPFLPRITTDNTTIEVEANGGVKSHMTYVRLNIA 120

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Db	121	KTEPKIRVRKAVLIIKRIKIOIEMI.KPELAPVSOLKYLRRRTVSTSMEEVNAKNNR	180
QY	181	DKNQTYNTLTGLDPFTEYVIALRCVAKESKFSWSDMSQEKMGMTIEEAPFCGLELMRYLKPAAE	240
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QY	241	ADGRPRVLLMKKAGAPYLEKTLGINMYEESNTNLTETMNTTNOOLEHLGGSEFVY	300
Db	241	ADGRPRVLLMKKAGAPYLEKTLGINMYEESNTNLTETMNTTNOOLEHLGGSEFVY	300
QY	301	SMISYNSLGKSEPAVLRIPIAIOEKSFQCIENVQACVAAEDQLVYKMOSSALDVNTWMIEMF	360
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QY	361	PDVDSSEPTLTSWESVSQATNMWTIQDDKLKPFWCYNISYVPM.LHDKVGEPEYSIOAYAKEGV	420
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QY	661	PEIPPRKSOYLRSRMEGSTRPEAKEQLLFSQSLVPDHLCEBAPNPYLKNSVTAREFLV	720
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DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	Gp130-like monocyte receptor.				
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OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
OX	NCBI_TaxID=10090;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=13988187; PubMed=11877449;				
RA	Ghiardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;				
RT	"A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signa				
RT	Proliferation, and Activates STAT-3 and STAT-5.";				
RL	J. Biol. Chem. 277:16831-16836(2002).				
DR	EMBL: AFB6621; AAM27959.1; -				
DR	MGD; MGI:2180511; GIMR.				
DR	InterPro: IPR002996; CRLA.				
DR	InterPro: IPR003961; FN_III.				
DR	Pfam: PF00041; fn03. 1.				
DR	SMART: SM00060; FN3. 3.				
DR	Receptor.				
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Query Match      54.6%; Score 2132.5; DB 11; Length 716;
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      61 GK-----SNVSDNATEASYSPFRSCAMPDPCSEVOAQNODGKVKSDITYMHLISI 112
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      113 AKTEPPIILISVNP1--CNRMFOIQW-KPREKTRGFPLVCMRLRFTVNSSKRTVEVNF---- 165
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      585 PAD--LIDKLIVNENLEVLVLTAEAGKQASILGEGANEVYTSPPRDPGPGKSFEP 642
Db      659 VSPRIIPRKSOYLRSMEPEGRPEAKQLLEFGSGS--LVPDHLCEEGAPNLYKNSVTAR 716
      643 ILTFVASEDSHSTCSRMADEAYSELARQPSSCSPGLSPPR--EDQAQNPLYKNSVTTR 700
QY      717 EFLVSEKLPEHTKGEV 732
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RESULT 4
Q9RS01 PRELIMINARY; PRT; 716 AA.
AC Q9RS01;
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DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cytokine receptor NR10.
GN GLMR OR NR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine
  receptor NR10."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083111; BAB88745.1; -.
MGD; MGI:2180511; Glimr.

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RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
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 DR HSSP; P40189; 180U.
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 DR Pfam: PF00041; fn3; 4.
 DR SMART: SMO060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 SO SEQUENCE 881 AA; 99003 MW; 7DE7942DD11138A0 CRC64;

Query Match	15.9%	Score 620.5;	DB 13;	Length 881;
Best Local Similarity	25.5%	Pred. No. 1.2e-40;		
Matches 194;	Conservative 123;	Mismatches 344;	Indels 101;	Gaps 23

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QY	74	TSERNASCFLPRTTIPDNTYITIEVEANGGVIKSHMTYWRLEMTIARTPEPKIRVPV	133
Db	174	-----SCTHSPGEQFIOTTFVYEARENELGIQSEFTLLIDPVNIYVNPQOLSELLS	227
QY	134	LGIRKMIQIEMIKPELAVSSDLKYTLREFTVNSTSMWEVNFAPKRRKDKNOTYNLTLQOP	193
Db	228	LELPNALKIEWKNP--ITNAPNLKYNIYRVPVKTQDW -EMVPEEDTASHRSOFTLQDLLP	284
QY	194	FTEVIALRCVAVKESK -FMSWSDQEKGMTDEEAPC -GLEIMRYLAPKEADAGRPRVLLM	251
Db	285	NTVYEVSEIYRCHKHKGHGHSWSDMSSELKQVTPREAPPSRDPDIWKLDSDPDANGNRPVIMTW	344
QY	252	KKARGAPLEKTLGYNIWYEPESNNTLJETNMNTYMOOLEHLHGSEFPWVMSIYSLKS	311
Db	345	KNLSDSVANGSILLIYSVFOGSOST---TENVICTSTYKTLISKRLYSVSYATVYRRAS	401
QY	312	PVALTRIPAIOEKSFQCIYV-----MQACVAEDOLVWQSSALDVTNMTIEMFPDVDS	366
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QY	487	KTSYIVOVMASTSAAGTNGTSINFKTISFYVEIITLITSLIGGILLIITLVAYGLKRP	546
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QY	547	NKLHLHLCMPYVNPAAESSIATW-----HGDDFKD-----KINLKES-DD	584
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QY	585	SVNTEDELRIKCPSTPSDKLVIDKLVANNGV-----LOETIFDEARTGQENNLGGEKN	637
Db	697	DIKSMDELKAKNTSEI-----LSSGIGGSSCLSSPRLASDCDEVESAOITTSSTVOYS	748
QY	638	GYVTCOPRPDPCPLGKSFEELEPVSEPIPRKSOYLRSRMEPTGRP---EAKQOLLESGQS	693
Db	749	TVIISGYBDQOP-----SAVIP-----HVFSR-SESQPLDCEERPEBHAGD-	791
QY	694	LVPDHLCEBEGAP---NPLYLKSIVAREP-----LYSEKLEPH	727
Db	792	-----KEGEPQAGNOYFKQNGCRHEDTNNKLQALHQBEPHS	826

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ID 057520	PRELIMINARY;	PRT; 710 AA
AC 057520;		
DT 01-JUN-1998	(TREMBLREL. 06, Created)	

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Gp130p3 (Fragment).
DE XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;

AN
RP
RC
RA
RT
RL

SEQUENCE FROM N.A.
TISSUE=Heart;
Chen J., Grace A., Chien K.R.;
"Partial characterization of putative Xenopus gp130";
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR HSP; P40189; 1B0U.
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DR InterPro; IPR003529; Hemtopoptn_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
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SQ SEQUENCE 710 AA: 79849 MW: BFA7C77E3B86CE6F CRC64;

Query Match	15.5%;	Score 606;	DB 13;	Length 710;
Best Local Similarity	25.5%;	Pred. No. 1.3e-39;		
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OY 137 KRMIOIEWIKPELAPVSSDLKYTLKRRYTNSTSMWEVNEAKNKEDKNQYVNLGLOPTE 196
Db 61 PNAKIKWMRNPLLNAPT--LKNIRRYPAKNDW-EMVPEEDTASHRDSPTLODILPYTE 117
OY 197 YIALRCANVKEK-FMSDMSQEKMGMTIEEARC-GELMRVLKPAADGRPRRLIMAKKA 254
Db 118 YEVSIARCLEDDEGRFMSDSEVKKOATPEAOPSRGPDVAKKIESPANGNREVMIMKML 177
OY 255 RGAPYLEKTLGYNIWYYPESTNLTETMTNTMOQLHHTGGESFEWFSMTISNLGSPVA 314
Db 178 SDSVANGKLLLYGVTFPOSSOST--TFNVTTTSYKTLTSLKDLXSYSVALYNGRASP8S 224
OY 315 TLRIIP---AIQKSFQECIEVMQACVAEDOLVVKMOSSALDYNWTMIEWEPDVDSPTT 369
Db 235 KINIPRSGNCPLDDEFR---VKTPREKELWEMTPEPNKSLDGXYIIECMKNYAQEGCI 290
OY 370 LSWESQAITNMTIQODKLPKPCVNIASVYPMHLKVGEPYSIQAAKGEVPSGEPTKY 429
Db 291 SDMQRTRNVNQTFLKGELEPLKCYIKRYLTKDCESVRSEAVLQOGTPLVGNHIT 350
OY 430 ENIGVKTWYITWKEIPKSEKGIICWYITFYQAGGKFSKYTNSSILQYGLSELRKTS 489
Db 351 KQVEKXRALLQMTVPVFDKRNGETIRNYITTYKSSHONASTAVVIDPDIETELSKEGNTL 410
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OY 550 THLCMPTVNPPESSITATW-----HDDKDKDLNLKESDSDVATEDRILIKPCS 597
Db 471 KKHIMPNDVDPKSNIAOMSPOTPSKHDENTKCHPRQDQSFYDVSAVEITAEHO-----K 525
OY 598 TFSDKLVIDLVLVNFQCNVLOEITFDEARTGOENLIGKNGVYTCFPR-----DCPLGK 652
Db 526 SFODIKSMPLKKN-----TSP-GSSGIGGS-----SCUSPLRSTSCDDEVE 568
OY 653 SFEEELPVSEITPPRKSQYLRSRMBEGRREAKFOLLFS-QGSLVPHLCE-----701
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OY 702 -BGAP---NPYLKNSVTAREFL--VSEKLEPHTKGEV 732
 DB 624 KESEPOGNOYFQKONCGLDEFTNKLQOEPSHIQOEL 660

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O8BN24 PRELIMINARY: PRT: 848 AA.
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 AC O8WN24:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Interleukin 12 receptor beta 2 chain (fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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 RA Solano-Aguller G.I., Zarlanga D.S., Beshah E., Vengroski K.,
 RA Gasparre L.C., Junker D., Cochran M., Weston C., Valencia D.,
 RA Chiang C., Lunney J.K.;
 RT "Limited effect of recombinant porcine interleukin-12 on porcine
 lymphocytes due to a low expression of IL-12 Beta2 receptor."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF48143; AAL60218.1;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 4.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
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 FT NON_TER
 FT SEQUENCE 848 AA; 94753 MW; AD66C885A27DA427 CRC64;

Query Match 11.0%; Score 430.5; DB 6; Length 848;
 Best Local Similarity 23.8%; Pred. No. 1.8e-25;
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OY 15 KFSLAALPAKPNISCVYR-YRKNLCTWSPCKETS-YTOYVVKRYAFGEHNDCTNS 72
 DB 106 ELSVAVPEQPNQVNSCMQKGERGYACSMDCRGDRHLYATVLLQLN--GPK--NLTYOK 160
 OY 73 STSE---NRASCSEFLPRITIPDNYTIEVEANGGVKSHMTYRLNIATKTEPKIFR 129
 DB 161 QCSDDYCCSLDGLNLPPESPSSYTAQVTAINSIGTASSFCFTLLDVAVRPLPMDIR 220
 OY 130 VKPVIGIKRMIOIEIKPELAVSSDLKYTLRFRTVNSTSMKEVNFANRKDKNOTYLT 189
 DB 221 IKCVNASMSTCTLQWRDEGLV-----LNLRLRYRVSYSRWNVN-ATNAKGR--HDLV 271
 OY 190 GLQPTTEVIALRCVAKESK-FWSDMSQKKMGTEEPACG-LELMRYLAKPAEADGRPV 247
 DB 272 DLKPTTEYFOISKPHLOKGRMSWSLSLTQTPKEKPTGLMDVWYKOHIDYV-ROOI 330
 OY 248 RLWK-----KARGAVLEKTLGYNIWYPPESNTNLTETMNTNOQLHLGSEFWVSM 302
 DB 331 SLFWKNLISSEARG-----KILHYQVTLQEVAGNATQNTIERSWMTIIPRTIYMAA 385
 OY 303 ISYNSLGSVPATLIPALQEKSPCIEVMAQVA-----EDOLVVKWOS- 347
 DB 386 VSAANSKSSSLPTR-----INIALDLCGAGLLAPOOVANPEGSIDLIVKWTSP 433
 OY 348 ---SALDVMTMMTEMPDVDS-----PTTLMSWSVSQATMMTIOQOKLRFWYINISV 398
 DB 434 GEGATAVEIYEW-----RELHLRGWQPLSPWRSPYNTSLISINIKPIYCEYELR 488
 OY 399 YPMHLDKVGEPTSIQAVAKGVSPSEPTKVENIGKTVITITWKEIPKSEKGIICNTI 458
 DB 489 HALSDQDGRS-SINGDLKHKAPLISGRPHINAISEKKSILISMDIIPAOEOMGCIILHYRI 547

OY 459 FYQAEQKGFGRK-----TVNSILIOYGLSLAKRRTSYIVQVMASTSAG-CTNGTSINF--- 510
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 DB 707 FRFPHNMPRGKQGLRQHNASEEDPSSASSPPRRALATGPAVDLYKVLGSR---- 762
 OY 640 VTCPRPDCPLCKSFEELPVSP-ELPPKRSOYLRSR--MREGTPR--EAKDQLPSCOS 693
 DB 763 -----RPDSKPGNPVSHLVLPVDYLPTEGYLPSNIDYLPHEAPITDSLEL----- 811
 OY 694 LVPDHLCGEGAPNPYLKNSVTAREFLVSRKL 724
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RESULT 10

O8MJS1 PRELIMINARY: PRT: 861 AA.
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 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Interleukin-12 receptor beta 2.
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 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kohno T.;
 RT "Cloning of porcine interleukin-12 receptor beta 2 gene."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF30213; AAM47543.1;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 3.
 DR SMART: SM00060; FN3; 4.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor.
 FT SEQUENCE 861 AA; 96055 MW; 2AB663E3C5F42534 CRC64;

Query Match 10.9%; Score 425.5; DB 6; Length 861;
 Best Local Similarity 24.3%; Pred. No. 4.8e-25;
 Matches 194; Conservative 109; Mismatches 339; Indels 157; Gaps 37;

OY 15 KFSLAALPAKPNISCVYR-YRKNLCTWSPCKETS-YTOYVVKRYAFGEHNDCTNS 72
 DB 117 ELSVAVPEQPNQVNSCMQKGERGYACSMDCRGDRHLYATVLLQLN--GPK--NLTYOK 171
 OY 73 STSE---NRASCSEFLPRITIPDNYTIEVEANGGVKSHMTYRLNIATKTEPKIFR 129
 DB 172 QCSDDYCCSLDGLNLPPESPSSYTAQVTAINSIGTASSLPSTFTFLDVAVRPLPMDIR 231
 OY 130 VKPVIGIKRMIOIEIKPELAVSSDLKYTLRFRTVNSTSMKEVNFANRKDKNOTYLT 189
 DB 232 IKCVNASVSTCTLQWRDEGLV-----LNLRLRYRVSYSRWNVN-ATNAKGR--HDLV 282
 OY 190 GLQPTTEVIALRCVAKESK-FWSDMSQKKMGTEEPACG-LELMRYLAKPAEADGRPV 247
 DB 283 DLKPTTEYFOISKPHLOKGRMSWSLSLTQTPKEKPTGLMDVWYKOHIDYK-ROOI 341
 OY 248 RLWK-----KARGAVLEKTLGYNIWYPPESNTNLTETMNTNOQLHLGSEFWVSM 302

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Db      342 SLFKNLSLSEARG-----KILHYOYTLQVEAGNATLQNTERNSTWTLPTGIMAAA 396
Oy      303 IS-INSLSKSPVATLRIPALQEKSPQCIEMQA-CVAEDOLVKKMQS---SALDNTMMI 357
Db      397 VSANSSKSSLPTRINLADLCAGILAPQOVSANDEGSDNLVWTKTSGBGATVAOEYV 456
Oy      358 EMFPDVDS-----PTTSMESVSQATNMTIQODKLKPPWCYNISVYPMILHKVGEPI 410
Db      457 EM-----RELHRLRGMOPLSLMSPRYNTSTLISDNKPYICYEIRHALISGQ-GGCS 510
Oy      411 SIQAAKEGVSESEPTKVENIGVTVITWKEIPKSERKGIICNTYITFOAEGGKFSK 470
Db      511 SIRDLKHKAPLSPHINAISEEKGSILISWDEIPAOQOMGCIILHYRIYKERDSDSQO 570
Oy      471 ----TVNSSILOYGLESILKRTSYIYOVMASAG-GINGNSINF---KITLSVFETIL 522
Db      571 LCEIPRYVSPKSHPNLSQPRVTYVLMWTLTAAGESPQGNRECECLOGKANWTF----- 626
Oy      523 ITSLIGGLILILITVAVGLK-----KPKKLTHLCWPTVPNPAESSIATWH 569
Db      627 ----VAPSLCAVITVGVFSMKRCRQKVFVLLALRP-----QMGSRITPDANS---TW- 674
Oy      570 GDDEKDKLNKESDSDSVNTEDEILKPCSTPS--DKLVIDKLNVF----- 612
Db      675 ----AKKYPVEEKQKSL-DRLADMTPEEPPELVINEVLPQVTPVFRPRHHNMPGK 729
Oy      613 GNVLOEIFTDEARQOENN-----LGGENGVYTCFRPDCPLG 651
Db      730 GORLOGRHASEDEGSSASSPPPPRALTAETGPAVDLYKVLGSR-----RDSKRG 780
Oy      652 KSFEELPVSP-EIPPRKSQYLRSRW---PEGTRP--EAKEQLLFSGSLVDPHLCSEAP 705
Db      781 NPVSLFLVLPVDYLPTHGTYLPSNMNDYLPSSHAPITDSLEEL-----PQHISLSVFP 832
Oy      706 NPYLKNSTAREFLVSEKL 724
Db      833 S-----NSLRLPLTFSCGCKL 847

RESULT 11
OyBEG2 ID 09BEG2 PRELIMINARY: PRT: 861 AA.
AC 09BEG2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE IL-12 receptor beta2 precursor.
GN IL-12R BETA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node;
RA Waldvogel A.S., Zahner A., Heussler V.T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ308426; CAC28320.1; -.
DR HSSP: P40189; IBCU.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_IL.
DR InterPro: IPR003529; Hemtopopctn_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS0153; HEMATOPO_REC_L_F2; 1.
DR Receptor: Signal.
FT SIGNAL 1
FT CHAIN 24 861 IL-12 RECEPTOR BETA2.
SQ SEQUENCE 861 AA: 96208 MW: 487B1E5D1E358E5B CRG64;

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Query Match

10.6%; Score 412.5; DB 6; Length 861;

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Best Local Similarity 24.1%; Pred. No. 5.2e-24;
Matches 195; Conservative 117; Mismatches 321; Indels 175; Gaps 40;

Oy      15 KESLAALPARKPENISCVYV-YRKNLCTWSPGKENS-YTOYTVKRTVAFGSKHNDCTNS 72
Db      117 EISGVVPEQPRNLSICQKGERGYTCWHGRDTHLTATYLLQ--GFR--NLWQK 171
Oy      73 STSE---NRASCSEFLPRTITPDNYTIEVEANGDVKISHMTYRLLENIAKTEPPKIFR 129
Db      172 QCNHCHQHDLDGINTLPRESLESSTYKVTAINSLGSSSPFESTLLDIYRPLRPMQIR 231
Oy      130 VKPVGLIKRMQIENIKELAPVSSDKYTLRFPTVNSTWMEVNF--AKNRKDKQTYN 187
Db      232 IKFVASVDRCTLLMRDEGLV-----LNLRLRYRPIINSRWMMVWVNAKGRHD----- 280
Oy      188 LTGQOPFEYVIALRCVAKESK-TWSDMSQEKMGTEEEAFCG-LELIRVLKPAEADGR 245
Db      281 LLDLKPFEYEFQISSKHLKGSWSMSLSRTQTPPEEPIGMANVMYMRQHDY-N-RQ 339
Oy      246 PVRLIMK-----KARGAVLEKTYGNIWYYPESNTNLETMTNTNQLLEHLHGSEFNV 300
Db      340 QISLFWKMLSSEARG-----KILHYOYTLQVAGGETTLQNTITHTSWTWIIPRTGMA 394
Oy      301 SMIS-YNSLGSVPATLRIPALQEKSFQCIEMQAQVAE-----DOLVVKW 345
Db      395 AAVSAANSKGS-----LPT-----RINTDLGAEALLAPQOVLAKSEGMDKLWYTW 441
Oy      346 ---QSSALDVNTMNIEM---FPDVSEPTTSLMESVSQATWNT-----IQODKLKFPW 392
Db      442 TPPEKATAAVOEYVEMRELHPGAGMOP-PLGM-----LMSPRYLSALISENIKPYI 493
Oy      393 CYNISVYPMILHDKVGEPEYSIAVAKEGVSESEPTKVENIGVTVITWKEIPKSERKGI 452
Db      494 CYEIVHALAGDQ-GGCSSTGNSSQHKAPLSPHINAISEKGSVLISMDLPAEQMG 552
Oy      453 ICNTYITFOAEGGK-----FSKTVNSSILOYGLESILKRTSYIYOVMASAG-GT 503
Db      553 ILHYRIYWKERDSNSQPOLCEIPRISPN-----HPIDSLQPRVTVYVLMWTLTAAGESP 608
Oy      504 NQTSINFKLSFVFEIILITSLIGGLILILITVAAGLKKPKNLTHL---CWPTVPN 559
Db      609 QGNREPEFLOGKANSTVAPSLCAVIMVGVLSMKRCRQKVFVLLALRPQWCSEKELP 668
Oy      560 PAESSIATWHDGDFDKLNKESDSDSVNTEDEILKPCSTPS--DKLVIDKLNVF----- 612
Db      669 PANS---TW-----AKKYPVEEKQK-LADRLLEWPTPEEPPELVINEVLCRTVPFR 719
Oy      613 -----GNVLOEIFTDE-----ARTGOENNLG---GEKNGVYTC 642
Db      720 PPHHRSWSEKGGGQVGHYTSSEDTGYSSASSPPPPAPATAETGQVDLYKVLGSKG----- 774
Oy      643 PRRPQPLGKSFEELPVSP-EIPPRKSQYLRSRW---PEGTRP--EAKEQLLFSGSLVP 696
Db      775 ---PDSKGNPASPLTILPVDYLPTHDGLPSNMNDYLPSSHAPITDPPEEL-----P 823
Oy      697 DHLCEGAPNPYLNSTAREFLVSEKL 724
Db      824 QHISLSTPS-----SLRLPLTFSCGCKL 847

RESULT 12
Oy0535 ID 070535 PRELIMINARY: PRT: 1093 AA.
AC 070535;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Leukemia inhibitor factor receptor alpha-chain.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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OY      112 TYRLENIATEPRKIFRVKPYVLGKRMQIMWIMELAPVSDJXTK-----LRRTV 165
      | : : |
Db      349 T-KVHV-----SHGNNTYLLCYVKLYGEV 372
OY      166 NSTSMWEVNEAKNRKDKNOTYNLTLGHOPEVEYVIALRCVAKESKF-MSDSOEOMGTEE 224
      | : : |
Db      373 IHEHNYSVHMSAN-----YLFSDLDPTKCYKAFRCVASANHHMKMSDMTKGFS-TPe 424
OY      225 EAPC-GLELMRVILKPAEADGRPRVRLIMKKAGAVLEKTLGYNIWYIPESNTNLTETM 263
      | : : |
Db      425 TAPSQALDVR-QVWSENGRRTVTLFPMPLKLSQANGKIISYNI--VVEEAKPTSEH 480
OY      284 -----TTNOOLEHLHGSEFWYMSISLNGKSPATLRIP-----ATOEKSPFCE 330
      | : : |
Db      481 YCVAPALSTNLSLD----QPYKIRITANNSMGSPESLAVLSDSHEKEXTIGT- 555
OY      331 VMOACVAEDOLVYKWOSSALDVNTVMIEFPDVSEPTTLSMESVS-QATNWTIQDQDK 369
      | : : |
Db      536 -----KAFNISMWPVSGDTMGVYVVMCAHSODORCDLQMKNLGPMTTSTTTSDFK 588
OY      390 PFWCYNISYVP-MLHBEKVGEPSIOAVYAKEGVPSGEPTEKVENIGVKTVITWKEIRKSE 448
      | : : |
Db      589 PGVRNYFRIFERKVEIKARLVKQGYQDELAPLVNPEVEIPISTPNSFVLKRFVDISDF 648
OY      449 RKGIICNVTLEFOA---EGKGFSKTV---NSSILOYL-----ESLKRKTSYIV 492
      | : : |
Db      649 QAGFIMGYLVYVSKEMQCNOCPMEWERTLLPDNSVLCCKYDINGSETKTLVENIWOESLYEF 708
OY      493 QVWASTSAG-GNGTGSINKT---LSFSVEFELLTSLIGGLLILILIVAYGLKRPNK 548
      | : : |
Db      709 FVTPYTSAGCPNRETFTKVTTPDARSHMLDQITLPMT-----LCVLLSIYCVW-KSQW 761
OY      549 LTHLCMPVYNPNAESSIATWGDDEKDK-----LNLEK-----S 582
      | : : |
Db      762 VKECXPDIPNPKYSIISL---IKSKKNPILIMWADCIPVLEVIYNAEBSKTCQVG 817
OY      583 DDSVNTEDILKRCSTPDSK-----LYIDKLVYN-----611
      | : : |
Db      818 SGLKLTIEDVPTKPIVPEKEDSSGVPCEIFENFTYDSDAFDSGHLIPQPLKDTAHL 877
OY      612 -----FGNVLOIEFTD---EARTGOENNLIGERKNYVCFPRPDCPLKSPFEEPLVS 660
      | : : |
Db      878 GLAPPNKQONVLKNDKMYMLVESTPEETSL-----YVSQLASPMC---GDKDTLATE 928
OY      661 PEIPEPKSOTLASRMEGT--RPEAKE 685
      | : : |
Db      929 PVPVHGSEKKRMVYVPGSLASPSLKE 955

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Search completed: August 4, 2003, 11:25:15
Job time : 117 secs
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